SEQUENCE LISTING

<110> Diversa Corporation
Kerovuo, Janne
Solbak, Arne
Gray, Kevin
McCann, Ryan
Purohit, Shalaka
Gerendash, Joel
Janssen, Giselle
Dahod, Samun

<120> PECTATE LYASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AND USING THEM

<130> 564462009640

<140> To Be Assigned
<141> Concurrently herewith

<150> 60/460,842
<151> 2003-04-04

<150> 60/484,798
<151> 2003-07-03

<160> 134

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1917
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

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120
acaattcaac aagcggtgga ccaggttccc aaagacaata cacacccggt cttgattcag
180
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240
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300
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360
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420
gaccgcgcga cgtttgaaaa ctgccggttc ctcggttggc aggacacttt gtttgtgaac
480
ggcagccgcc acttcttcaa agactgctac gtcgaaggcc acgtcgattt cattttcggc
540
acggcctccg ccgtgtttga gaactgcacc attcacagca aaggcgaagg ttatgtgacc

600
gcacactatc gcaccagcga tgagatggat accggttttg tctttcatcg ttgtcgtttg
660
accggacgag acacgggccg cggagtttat ctcggaaggc cttggcgacc ttacgcgcgc
720
gtcgtcttta tcgattgctg gctggacgca cacatcagac ctgaaggctg ggataattgg
780
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840
gctaatcccg tagctcgtgt cgcgtggtcc aggcagttga cgacagaaca agccgccgag
900
ttttcgcggg aacgcttttt cagccgcgct gttcgcgggc tctctgggca ggccaaccag
960
gcagtcggaa cgatcgcgtg ggacgatgcg cagaaaaaac cgaacgagtg gtatgcgagc
1020
gccgaggcgt tgcgcattgc cgacaacgtt gttctttatc aacgtgactc cggcggttgg
1080
cccaagaaca tcgacatggg gaagccgctc gacgaaaagg gtcgagccgg tcttctgcgc
1140
gtgcgtaaga agaacgattc cacgatcgac aatggcgcga cttacacgca actctcgttt
1200
ctggcgcggg tttacacggc gcaaaagcag gagcggcatc gcgagtcgtt tctgaaggga
1260
ctcgattacc tgttgaaggc gcagtatcca aacggaggct ggccgcagtt ctatcccaac
1320
ctcaacggct attacaaaca catcactttc aacgacaacg ccatgatcgg cgtgatgaaa
1380
ctgctgcgcg acgtagcgac agcgaaaccg gcgtatgcgt tcgtcgacga agcacgacgg
1440
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1500
gtgaatggcc ggcgcaccgt gtggtgtgcg caacatgacg aagtcacgct cgcgcctgcc
1560
ccggcgagga cgtttgaatt agtttcgctg agtggtggtg aaagcgttga gatcgtgcgc
1620
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1680
gcgtggttcg agcaatcgca agtgaaagat cccgccggca aacctgcgtg ggcgcgattt
1740
tatgagatcg gcactaatcg tccgatcttc gccgggcgtg acggcgtcgt taagtatgat
1800
gtgaaacaga tcgatgagga acgacgaaag aattacgcat ggtacgttga cgacgcagcg
1860
aaactactga aaaccgacta tcctgagtgg aaagaaaaga acgccaaaga tcaatga
1917

<210> 2
<211> 638
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(21)

<221> DOMAIN
<222> (28)...(308)
<223> Pectin methyl esterase domain

<221> DOMAIN
<222> (309)...(638)
<223> Catalytic domain

<400> 2

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Ala Asp Gly Ser Gly Asp Val Arg Thr Ile Gln Gln Ala Val Asp Gln
        35                  40                  45
Val Pro Lys Asp Asn Thr His Pro Val Leu Ile Gln Ile Lys Pro Gly
    50                  55                  60
Val Tyr Gln Glu Gln Val Arg Val Ala Ala Gly Lys Arg Phe Ile Thr
65                  70                  75                  80
Phe Arg Gly Asp Asp Ala Ser Lys Thr Val Ile Thr Tyr Arg Leu Ser
                85                  90                  95
Ala Leu Gln Ala Gly Asn Thr Arg Leu Ala Phe Thr Thr Phe Val Asn
            100                 105                 110
Ala Asp Asp Phe Arg Ala Glu Asn Leu Thr Phe Glu Asn Ser Phe Gly
        115                 120                 125
Thr Gly Ser Gln Ala Val Ala Leu Phe Val Asp Ala Asp Arg Ala Thr
    130                 135                 140
Phe Glu Asn Cys Arg Phe Leu Gly Trp Gln Asp Thr Leu Phe Val Asn
145                 150                 155                 160
Gly Ser Arg His Phe Phe Lys Asp Cys Tyr Val Glu Gly His Val Asp
                165                 170                 175
Phe Ile Phe Gly Thr Ala Ser Ala Val Phe Glu Asn Cys Thr Ile His
            180                 185                 190
Ser Lys Gly Glu Gly Tyr Val Thr Ala His Tyr Arg Thr Ser Asp Glu
        195                 200                 205
Met Asp Thr Gly Phe Val Phe His Arg Cys Arg Leu Thr Gly Arg Asp
    210                 215                 220
Thr Gly Arg Gly Val Tyr Leu Gly Arg Pro Trp Arg Pro Tyr Ala Arg
225                 230                 235                 240
Val Val Phe Ile Asp Cys Trp Leu Asp Ala His Ile Arg Pro Glu Gly
                245                 250                 255
Trp Asp Asn Trp Arg Asp Pro Glu Arg Glu Lys Thr Ala Trp Phe Ala
            260                 265                 270
Glu Tyr Lys Ser Lys Gly Pro Gly Ala Asn Pro Val Ala Arg Val Ala
        275                 280                 285
Trp Ser Arg Gln Leu Thr Thr Glu Gln Ala Ala Glu Phe Ser Arg Glu
    290                 295                 300
Arg Phe Phe Ser Arg Ala Val Arg Gly Leu Ser Gly Gln Ala Asn Gln
305                 310                 315                 320
Ala Val Gly Thr Ile Ala Trp Asp Asp Ala Gln Lys Lys Pro Asn Glu
                325                 330                 335
Trp Tyr Ala Ser Ala Glu Ala Leu Arg Ile Ala Asp Asn Val Val Leu
            340                 345                 350
Tyr Gln Arg Asp Ser Gly Gly Trp Pro Lys Asn Ile Asp Met Gly Lys
        355                 360                 365
Pro Leu Asp Glu Lys Gly Arg Ala Gly Leu Leu Arg Val Arg Lys Lys
    370                 375                 380
Asn Asp Ser Thr Ile Asp Asn Gly Ala Thr Tyr Thr Gln Leu Ser Phe
385                 390                 395                 400
Leu Ala Arg Val Tyr Thr Ala Gln Lys Gln Glu Arg His Arg Glu Ser
                405                 410                 415
Phe Leu Lys Gly Leu Asp Tyr Leu Leu Lys Ala Gln Tyr Pro Asn Gly
            420                 425                 430
Gly Trp Pro Gln Phe Tyr Pro Asn Leu Asn Gly Tyr Tyr Lys His Ile
        435                 440                 445
```

Thr Phe Asn Asp Asn Ala Met Ile Gly Val Met Lys Leu Leu Arg Asp
450 455 460
Val Ala Thr Ala Lys Pro Ala Tyr Ala Phe Val Asp Glu Ala Arg Arg
465 470 475 480
Thr Ser Ala Ala Lys Ala Val Glu Lys Gly Ile Glu Cys Ile Leu Lys
485 490 495
Thr Gln Val Val Val Asn Gly Arg Arg Thr Val Trp Cys Ala Gln His
500 505 510
Asp Glu Val Thr Leu Ala Pro Ala Pro Ala Arg Thr Phe Glu Leu Val
515 520 525
Ser Leu Ser Gly Gly Glu Ser Val Glu Ile Val Arg Phe Leu Met Ser
530 535 540
Ile Lys Asn Pro Ser Pro Ala Val Val Glu Ala Ile Glu Ser Ala Val
545 550 555 560
Ala Trp Phe Glu Gln Ser Gln Val Lys Asp Pro Ala Gly Lys Pro Ala
565 570 575
Trp Ala Arg Phe Tyr Glu Ile Gly Thr Asn Arg Pro Ile Phe Ala Gly
580 585 590
Arg Asp Gly Val Val Lys Tyr Asp Val Lys Gln Ile Asp Glu Glu Arg
595 600 605
Arg Lys Asn Tyr Ala Trp Tyr Val Asp Asp Ala Ala Lys Leu Leu Lys
610 615 620
Thr Asp Tyr Pro Glu Trp Lys Glu Lys Asn Ala Lys Asp Gln
625 630 635

<210> 3
<211> 1416
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 3
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gcgccgcgtc tgtctgcgtt tgcagcggag gagaatccgt gggaaacggt gatgccttcg
120
atcgtgaaac gcatcaagcg acctcgtttc ccgatgcgca cgtttgatct cacggagttt
180
ggagcgaaag gtgatggacg aacagattgc acgttggctt tccgtcgcgc gatcgatcga
240
tgcacgaacg ccggtggtgg gagagtagtt gttccaccgg gttcgtatct cactggcgcc
300
attcatttga agagcaacgt cgaccttcat atctcagaag gtactacggt caagttcagc
360
cagaacccga aagactacct gcccgttgtt ttctcgcgtt gggaaggcgt cgaggtgttc
420
aactactcgc cttttatcta cgccttcgaa caaacgaaca ttgcgatcac tggcaagggc
480
acgctcaacg gtcaaagcga caacgaacac tggtggccct ggaacggacg tgccgcgtac
540
ggctggaaag aagggatgag caatcagcgt cccgatcgaa atgcgctgtt tgcgatggcc
600
gaaaaaggtg tcccggttca ggagcgcatt tttggtgagg gccattactt aaggccgcag
660
ttcattcaac cttatcgttg tgagaacgtg ctgatcgaag gtgtcactat tcgaaactcg
720
ccgatgtggg aaattcatcc ggtgctctgc cggaatgtca tcgtccaaaa tgtgatcatc
780
aacagtcatg gtccaaacaa cgacgggtgt aatcctgagt cgtgcacgga tgtgttgatt

840
aaggattgtg acttcgacac tggtgacgat tgtatcgcga tcaagtcagg ccgaaatgca
900
gatgggcggc gactgaaggc tcctactgaa aacattatcg tgactggttg tcgcatgaaa
960
gatggtcacg gcgggattac ggtgggcagc gagatttcgg gtggggtgcg aaatcttttc
1020
gcatccaact gccggctcga cagtccgaac ctggaccatg cattgcgggt taagaataac
1080
gctatgcgtg gcgggctgtt ggagaatctg cacttccgaa atatcgacgt cgggcaagtg
1140
gcgcacgcgg tgatcacgat cgatttcaat tatgaggaag gcgcgaaggg atcgttcacg
1200
ccagtcgttc gtgattacac cgtcgatggc cttcgcagca cgaaaagtaa gtacgcgctc
1260
gatgtgcagg gcttggcgac ggcgccgatc gtgaatctgc gtctaaccaa ctgcatcttc
1320
gacaatgtcg ctgaaggaaa tgttgtgaag aacgtaaagg atgcaactat cgagaatgtc
1380
aaaatcaatg gaaaaagcgt tgatgcagtg ccgtag
1416

<210> 4
<211> 471
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(28)

<221> DOMAIN
<222> (81)...(476)
<223> Catalytic domain

<400> 4
Met Ser Ser Arg Arg Glu Phe Ile Arg Asp Leu Leu Thr Gly Gly Ala
 1   5   10   15
Leu Ile Ala Val Ala Pro Arg Leu Ser Ala Phe Ala Ala Glu Glu Asn
            20   25   30
Pro Trp Glu Thr Val Met Pro Ser Ile Val Lys Arg Ile Lys Arg Pro
        35   40   45
Arg Phe Pro Met Arg Thr Phe Asp Leu Thr Glu Phe Gly Ala Lys Gly
    50   55   60
Asp Gly Arg Thr Asp Cys Thr Leu Ala Phe Arg Arg Ala Ile Asp Arg
65   70   75   80
Cys Thr Asn Ala Gly Gly Gly Arg Val Val Val Pro Pro Gly Ser Tyr
                85   90   95
Leu Thr Gly Ala Ile His Leu Lys Ser Asn Val Asp Leu His Ile Ser
            100   105   110
Glu Gly Thr Thr Val Lys Phe Ser Gln Asn Pro Lys Asp Tyr Leu Pro
        115   120   125
Val Val Phe Ser Arg Trp Glu Gly Val Glu Val Phe Asn Tyr Ser Pro
    130   135   140
Phe Ile Tyr Ala Phe Glu Gln Thr Asn Ile Ala Ile Thr Gly Lys Gly
145   150   155   160
Thr Leu Asn Gly Gln Ser Asp Asn Glu His Trp Trp Pro Trp Asn Gly
                165   170   175
Arg Ala Ala Tyr Gly Trp Lys Glu Gly Met Ser Asn Gln Arg Pro Asp

```
            180                 185                 190
Arg Asn Ala Leu Phe Ala Met Ala Glu Lys Gly Val Pro Val Gln Glu
        195                 200                 205
Arg Ile Phe Gly Glu Gly His Tyr Leu Arg Pro Gln Phe Ile Gln Pro
    210                 215                 220
Tyr Arg Cys Glu Asn Val Leu Ile Glu Gly Val Thr Ile Arg Asn Ser
225                 230                 235                 240
Pro Met Trp Glu Ile His Pro Val Leu Cys Arg Asn Val Ile Val Gln
                245                 250                 255
Asn Val Ile Ile Asn Ser His Gly Pro Asn Asn Asp Gly Cys Asn Pro
            260                 265                 270
Glu Ser Cys Thr Asp Val Leu Ile Lys Asp Cys Asp Phe Asp Thr Gly
        275                 280                 285
Asp Asp Cys Ile Ala Ile Lys Ser Gly Arg Asn Ala Asp Gly Arg Arg
    290                 295                 300
Leu Lys Ala Pro Thr Glu Asn Ile Ile Val Thr Gly Cys Arg Met Lys
305                 310                 315                 320
Asp Gly His Gly Gly Ile Thr Val Gly Ser Glu Ile Ser Gly Gly Val
                325                 330                 335
Arg Asn Leu Phe Ala Ser Asn Cys Arg Leu Asp Ser Pro Asn Leu Asp
            340                 345                 350
His Ala Leu Arg Val Lys Asn Asn Ala Met Arg Gly Gly Leu Leu Glu
        355                 360                 365
Asn Leu His Phe Arg Asn Ile Asp Val Gly Gln Val Ala His Ala Val
    370                 375                 380
Ile Thr Ile Asp Phe Asn Tyr Glu Glu Gly Ala Lys Gly Ser Phe Thr
385                 390                 395                 400
Pro Val Val Arg Asp Tyr Thr Val Asp Gly Leu Arg Ser Thr Lys Ser
                405                 410                 415
Lys Tyr Ala Leu Asp Val Gln Gly Leu Ala Thr Ala Pro Ile Val Asn
            420                 425                 430
Leu Arg Leu Thr Asn Cys Ile Phe Asp Asn Val Ala Glu Gly Asn Val
        435                 440                 445
Val Lys Asn Val Lys Asp Ala Thr Ile Glu Asn Val Lys Ile Asn Gly
    450                 455                 460
Lys Ser Val Asp Ala Val Pro
465                 470
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<210> 5
<211> 1077
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 5
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attctaaagc agccgaaact ttggtacgcg gtcgacgaag cgacgcggat cgcaaatcag
120
gtgatccttt atcaacgcga caacggtggt tggccgaaga atatcgacat ggccgccatg
180
ctcatgcagg cagaacgcga aaaacttagt cgcgagaaga gcgagaccga cacgacaatc
240
gacaacggcg cgacgacaac ccagctcgcg tatctggcga aggtcatcac ggccaagaat
300
atcgaaagcc atcgcgtcgc gtttttcaaa ggcctcgatt ttcttttcgc catgcagtac
360
gggaatggcg gcttcccgca atttttcct ctgcgtgacg attattcgcg cgagattacg
420

ttcaacgaca acgcgatgat aaatgtgctt cggttgctcc gcgacatagc cgatcgaaag
480
aacgattatg tgtttgtcga tgaagagcgg cgagcgaagg ccgagcaggc tgtaaggcgt
540
gcgatcccgt tgatcctcag cacgcaggtc gtcgtcgatg gaaagaaaac cgtctgggct
600
gcgcagtatg atgagaagac attgaagccg gccgcggcgc gaaagttcga gccggcatca
660
ttgaccgccg gcgagagcgt tggcatcgtc cggtttttga tgctagaaaa accaacaccc
720
gagatcatta acgcgatcga atccgccatc gcttggtaca aggcgaacaa catctcggga
780
cttaggtggg agaggcgaaa cggcgagaac attgtgatca aagacaagaa cgcgccgccc
840
gtctgggcgc gcttttatca gatcgaaacg atgaggccga tcttcgccgg tcgcgatgcg
900
gtcatcagat acgatgtgat gcagatcgag tcggaacgtc gaaacggata tgcatggtac
960
gtatccgaac cgaatgagtt gttgaatgaa gattatccga agtggaggac aaggagtgcg
1020
aagcgtgccc agatctttca acgtccgcct cttggttcga gatttcggac cgtgtag
1077

<210> 6
<211> 358
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(358)
<223> Catalytic domain

<400> 6
Met Asp Asp Lys Trp Ala Glu Arg Thr Ser Pro Asp Phe Asn Leu Val
 1   5   10   15
Ser Trp Asn Glu Ile Leu Lys Gln Pro Lys Leu Trp Tyr Ala Val Asp
            20   25   30
Glu Ala Thr Arg Ile Ala Asn Gln Val Ile Leu Tyr Gln Arg Asp Asn
        35   40   45
Gly Gly Trp Pro Lys Asn Ile Asp Met Ala Ala Met Leu Met Gln Ala
    50   55   60
Glu Arg Glu Lys Leu Ser Arg Glu Lys Ser Glu Thr Asp Thr Thr Ile
65   70   75   80
Asp Asn Gly Ala Thr Thr Thr Gln Leu Ala Tyr Leu Ala Lys Val Ile
                85   90   95
Thr Ala Lys Asn Ile Glu Ser His Arg Val Ala Phe Phe Lys Gly Leu
            100   105   110
Asp Phe Leu Phe Ala Met Gln Tyr Gly Asn Gly Gly Phe Pro Gln Phe
        115   120   125
Phe Pro Leu Arg Asp Asp Tyr Ser Arg Glu Ile Thr Phe Asn Asp Asn
    130   135   140
Ala Met Ile Asn Val Leu Arg Leu Leu Arg Asp Ile Ala Asp Arg Lys
145   150   155   160
Asn Asp Tyr Val Phe Val Asp Glu Glu Arg Arg Ala Lys Ala Glu Gln
                165   170   175
Ala Val Arg Arg Ala Ile Pro Leu Ile Leu Ser Thr Gln Val Val Val
            180   185   190
Asp Gly Lys Lys Thr Val Trp Ala Ala Gln Tyr Asp Glu Lys Thr Leu

```
        195                 200                 205
Lys Pro Ala Ala Ala Arg Lys Phe Glu Pro Ala Ser Leu Thr Ala Gly
    210                 215                 220
Glu Ser Val Gly Ile Val Arg Phe Leu Met Leu Glu Lys Pro Thr Pro
225                 230                 235                 240
Glu Ile Ile Asn Ala Ile Glu Ser Ala Ile Ala Trp Tyr Lys Ala Asn
                245                 250                 255
Asn Ile Ser Gly Leu Arg Trp Glu Arg Arg Asn Gly Glu Asn Ile Val
            260                 265                 270
Ile Lys Asp Lys Asn Ala Pro Pro Val Trp Ala Arg Phe Tyr Gln Ile
        275                 280                 285
Glu Thr Met Arg Pro Ile Phe Ala Gly Arg Asp Ala Val Ile Arg Tyr
    290                 295                 300
Asp Val Met Gln Ile Glu Ser Glu Arg Arg Asn Gly Tyr Ala Trp Tyr
305                 310                 315                 320
Val Ser Glu Pro Asn Glu Leu Leu Asn Glu Asp Tyr Pro Lys Trp Arg
                325                 330                 335
Thr Arg Ser Ala Lys Arg Ala Gln Ile Phe Gln Arg Pro Pro Leu Gly
            340                 345                 350
Ser Arg Phe Arg Thr Val
        355
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<210> 7
<211> 1125
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

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gcgcggctct cccgaaccat tccgtcctcg ccggcgcaga gcgctgcggt cagcggggtt
120
ccggcggcga tccgctgggg agcggacgtc ctgcggcaga agccggagtg gtatgcctcg
180
cgagaggcga ggacgatcgc cgacagcgtc atccagtacc aggcggcgga cggcggctgg
240
cccaagaaca ccgacctcgg gactccgccc acggctgaat cacgcgccgg cgcggcggcc
300
gacgtgacgt cgagcaccat cgacaacaac ggcacgacga tgccgatgca gttccttgcg
360
ctggtggcgg acgcgaccgg cgaggctcgc tatcgcgcgt cgttcctccg cggcttcgac
420
tacctgctcg ccgcgcagta tcccaacggc ggctggccgc agttctttcc gctccgccgc
480
gggtattaca cccacatcac cttcaacgac aacgcgatgg tcaacgtgct gaccgtgctg
540
cgcgatgccg cggccggtca ggcgccatac gccttcgtgg acgagccccg ccgcgcgaag
600
gcccgcgccg ccgtgtcccg ggggatcgac gtcatcctga agacccaagt gaaacagaac
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ggcaagctga cggcgtggtg cgcgcagcac gacgagaaga ccctcgcgcc ggcgtgggcg
720
cgcgcttacg agccgccatc gctctccggc agcgaaaccg tcggcatcgt ccgcttcctg
780
atggagatcg agaagccgtc accggagatc gtcgccgcga tcgaaggggc cgtcgcctgg
840
ctgaagtccg tggcgattcc ggggctgcgc tacgagtcct tcaccggcgc ggacggacag
900

agggaccgcc gcgtcgttcc ggatccatcg gccggactcc tgtgggcgcg gttctacgag
960
ctcggcacca accggccgat cttcctcggc cgcgactccg tggttcgcgc cgcgctcagt
1020
gacatcgaac gcgagcgccg cgccggctac gcctactacg gtacgtggcc ggcgagcctg
1080
attgctgcgg actacccgcg ctggcgttcg acgctccggc gctga
1125

<210> 8
<211> 374
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(374)
<223> Catalytic domain

<400> 8
Met His Ala Gly Ala Lys His Val Ser Arg Trp Arg Glu Glu Phe Leu
 1   5   10   15
Arg Asp Phe Ala Ala Arg Leu Ser Arg Thr Ile Pro Ser Ser Pro Ala
            20   25   30
Gln Ser Ala Ala Val Ser Gly Val Pro Ala Ala Ile Arg Trp Gly Ala
        35   40   45
Asp Val Leu Arg Gln Lys Pro Glu Trp Tyr Ala Ser Arg Glu Ala Arg
    50   55   60
Thr Ile Ala Asp Ser Val Ile Gln Tyr Gln Ala Ala Asp Gly Gly Trp
65   70   75   80
Pro Lys Asn Thr Asp Leu Gly Thr Pro Pro Thr Ala Glu Ser Arg Ala
                85   90   95
Gly Ala Ala Ala Asp Val Thr Ser Ser Thr Ile Asp Asn Asn Gly Thr
            100   105   110
Thr Met Pro Met Gln Phe Leu Ala Leu Val Ala Asp Ala Thr Gly Glu
        115   120   125
Ala Arg Tyr Arg Ala Ser Phe Leu Arg Gly Phe Asp Tyr Leu Leu Ala
    130   135   140
Ala Gln Tyr Pro Asn Gly Gly Trp Pro Gln Phe Phe Pro Leu Arg Arg
145   150   155   160
Gly Tyr Tyr Thr His Ile Thr Phe Asn Asp Asn Ala Met Val Asn Val
                165   170   175
Leu Thr Val Leu Arg Asp Ala Ala Ala Gly Gln Ala Pro Tyr Ala Phe
            180   185   190
Val Asp Glu Pro Arg Arg Ala Lys Ala Arg Ala Ala Val Ser Arg Gly
        195   200   205
Ile Asp Val Ile Leu Lys Thr Gln Val Lys Gln Asn Gly Lys Leu Thr
    210   215   220
Ala Trp Cys Ala Gln His Asp Glu Lys Thr Leu Ala Pro Ala Trp Ala
225   230   235   240
Arg Ala Tyr Glu Pro Pro Ser Leu Ser Gly Ser Glu Thr Val Gly Ile
                245   250   255
Val Arg Phe Leu Met Glu Ile Glu Lys Pro Ser Pro Glu Ile Val Ala
            260   265   270
Ala Ile Glu Gly Ala Val Ala Trp Leu Lys Ser Val Ala Ile Pro Gly
        275   280   285
Leu Arg Tyr Glu Ser Phe Thr Gly Ala Asp Gly Gln Arg Asp Arg Arg
    290   295   300
Val Val Pro Asp Pro Ser Ala Gly Leu Leu Trp Ala Arg Phe Tyr Glu

305 310 315 320
Leu Gly Thr Asn Arg Pro Ile Phe Leu Gly Arg Asp Ser Val Val Arg
325 330 335
Ala Ala Leu Ser Asp Ile Glu Arg Glu Arg Arg Ala Gly Tyr Ala Tyr
340 345 350
Tyr Gly Thr Trp Pro Ala Ser Leu Ile Ala Ala Asp Tyr Pro Arg Trp
355 360 365
Arg Ser Thr Leu Arg Arg
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<210> 9
<211> 1116
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 9
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ctgctctttg cggcagccac acagggaacc aagccgcccg aagtgcggtg gaatgagtgc
120
ctaaaccaaa aacctgcctg gtacggcagc ccggaagcgg tgcgcattgc tgacaacctg
180
ttgctttacc aacgcgacca cggcggctgg cacaagaata tcgaaatggc tgcggtcttg
240
accgaacagc aacaggcaga gttgaaagcg caaaaggcaa ccgacgattc gacgattgat
300
aacggcgcga cctataccca ggtgatttat ctggcgcgcg tcttcaatgc gacgaagcag
360
gagcgattca aaaccgcgtt tctcaaagga ttcgattatc tgctcaaggc tcagtatgcg
420
aacggcggct ggccgcagta ttacccgcgt ttgcagggtt attacaaaca catcacgttc
480
aacgatgacg cgatggtcgg cgtgcttgat cttctgcgcg atgttgcgcg cggcgattcc
540
ggttatcggt tcgtggacag cgaccggcgc gcccgcgcca gccaggccgt gcaaaaagga
600
attgagtgca tcttgaaatg ccagatcgtg gtcgccggga aaaagaccgc ctggtgcgcg
660
caacacgatg aagtgacatt cgcccccgcg ccggcacgca cctacgagaa aatttcgctg
720
agcggcagcg aatcggttgg cctgatccgc ttcctgatgg gcattgaaca accggacgcg
780
cgtgtagttg aggcgattga gtccgccgtt gcctggctca agcaagccaa gctgaccggc
840
atcaaagtgg ttcagaaggc ggatgcttcg aagcccaatg gcttcgaccg ggtcgtcgtt
900
gaagatgcac aagccgggcc attgtgggcg cgcttttacg agatcggtac gggccgcccg
960
atcttttccg gacgtgacgg catcgtcaaa tacagcttgg cggaaatcga acacgaacgg
1020
cgcacgggct acggctggta cacgaatgcg cccgcgaaat tgctggaaca agattatccg
1080
gcctggcaaa tcaaacgcgg gggcaagaaa aagtaa
1116

<210> 10
<211> 371
<212> PRT

<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(29)

<221> DOMAIN
<222> (30)...(371)
<223> Catalytic domain

<400> 10

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Met Ile Gly Ser Met Lys Thr Ile Leu Ser Asn Leu Asn Ala Ala Leu
 1               5                  10                  15
Leu Ser Cys Ala Leu Leu Phe Ala Ala Ala Thr Gln Gly Thr Lys Pro
            20                  25                  30
Pro Glu Val Arg Trp Asn Glu Cys Leu Asn Gln Lys Pro Ala Trp Tyr
        35                  40                  45
Gly Ser Pro Glu Ala Val Arg Ile Ala Asp Asn Leu Leu Leu Tyr Gln
    50                  55                  60
Arg Asp His Gly Gly Trp His Lys Asn Ile Glu Met Ala Ala Val Leu
65                  70                  75                  80
Thr Glu Gln Gln Gln Ala Glu Leu Lys Ala Gln Lys Ala Thr Asp Asp
                85                  90                  95
Ser Thr Ile Asp Asn Gly Ala Thr Tyr Thr Gln Val Ile Tyr Leu Ala
            100                 105                 110
Arg Val Phe Asn Ala Thr Lys Gln Glu Arg Phe Lys Thr Ala Phe Leu
        115                 120                 125
Lys Gly Phe Asp Tyr Leu Leu Lys Ala Gln Tyr Ala Asn Gly Gly Trp
    130                 135                 140
Pro Gln Tyr Tyr Pro Arg Leu Gln Gly Tyr Tyr Lys His Ile Thr Phe
145                 150                 155                 160
Asn Asp Asp Ala Met Val Gly Val Leu Asp Leu Leu Arg Asp Val Ala
                165                 170                 175
Arg Gly Asp Ser Gly Tyr Arg Phe Val Asp Ser Asp Arg Arg Ala Arg
            180                 185                 190
Ala Ser Gln Ala Val Gln Lys Gly Ile Glu Cys Ile Leu Lys Cys Gln
        195                 200                 205
Ile Val Val Ala Gly Lys Lys Thr Ala Trp Cys Ala Gln His Asp Glu
    210                 215                 220
Val Thr Phe Ala Pro Ala Pro Ala Arg Thr Tyr Glu Lys Ile Ser Leu
225                 230                 235                 240
Ser Gly Ser Glu Ser Val Gly Leu Ile Arg Phe Leu Met Gly Ile Glu
                245                 250                 255
Gln Pro Asp Ala Arg Val Val Glu Ala Ile Glu Ser Ala Val Ala Trp
            260                 265                 270
Leu Lys Gln Ala Lys Leu Thr Gly Ile Lys Val Val Gln Lys Ala Asp
        275                 280                 285
Ala Ser Lys Pro Asn Gly Phe Asp Arg Val Val Val Glu Asp Ala Gln
    290                 295                 300
Ala Gly Pro Leu Trp Ala Arg Phe Tyr Glu Ile Gly Thr Gly Arg Pro
305                 310                 315                 320
Ile Phe Ser Gly Arg Asp Gly Ile Val Lys Tyr Ser Leu Ala Glu Ile
                325                 330                 335
Glu His Glu Arg Arg Thr Gly Tyr Gly Trp Tyr Thr Asn Ala Pro Ala
            340                 345                 350
Lys Leu Leu Glu Gln Asp Tyr Pro Ala Trp Gln Ile Lys Arg Gly Gly
        355                 360                 365
Lys Lys Lys
    370
```

<210> 11
<211> 1167
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 11
atgtcgttgg gaccaggtgc taatccgaaa gctcgcgttc cctggtccaa acaactatcg
60
ggtgttgagg caaagttgtt cgatcgcgag cggttcttca gcctcgctgc ggaacgaacc
120
tctaagaaga atgaccagca agtcggcgcc atcgcgtgga aagatgcaca cggaaaggca
180
gatgagtggt atgcgagcgt tgaggcactt cgtatagccg ataacgtcgt tttctatcaa
240
cgtgactcag gtggctggcc caagaatatc gagatggcga agacgttgag cgatcgtgag
300
aaggctgcga ttctccgcga gaagaaaaag aatgactcaa caatcgacaa tggcgcgact
360
cacactcagt tatcttttct ggcgcgcgtc tatacagcac aacagcagga gcgacatcgc
420
gagtcatttt taaaaggact ggattactta ctgaaggcgc agtattcaaa tggtggctgg
480
ccacagttct atccaaactt gaatggctac tacaaacgga tcacgtacaa cgatggcgcg
540
atgatcggtg tgatgaagct tctgcgtgat gttgcggcag cgaaacctga atacgcgttt
600
gtcgatgaaa ctcggcgtgc gaaggctgcg aacgcggtgg aaaaaggcat cgtgtgcatt
660
ttgaaaacgc aggtggttgt tgatgggcgt cgcactgttt ggtgtgcaca acacgacgaa
720
gtgacgtttg cgcccgcgcc tgcaagaaag tttgagttag cttcgttgag cggcggtgag
780
agcgtcgata ttgttcgatt tctaatgtcg ataaaggatc catcgcgtaa cgtggttgaa
840
tcgattgaat cggcagttaa atggtttgag cagtcggagc taaaaggcgt taagtgggtc
900
aagaaaaccg acgctactca acctaatggg ttcgattgtg tcgttgttaa agatccggag
960
agctctgttt gggcgcgctt ttacgagatt ggcacgaacc gcccgatctt tgccgggcgt
1020
gatggagtgc ctaagtatga cgtcgcgcag atcgaacacg agcgacgaac gggttacgaa
1080
tggtacgttg atgaggcagc aaaactgctg aaaaaagatt atccggcgtg gaagaaacga
1140
catgtcgtca cgacgcgagt tcattag
1167

<210> 12
<211> 388
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(388)

<223> Catalytic domain

<400> 12

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Met Ser Leu Gly Pro Gly Ala Asn Pro Lys Ala Arg Val Pro Trp Ser
 1               5                  10                  15
Lys Gln Leu Ser Gly Val Glu Ala Lys Leu Phe Asp Arg Glu Arg Phe
            20                  25                  30
Phe Ser Leu Ala Ala Glu Arg Thr Ser Lys Lys Asn Asp Gln Gln Val
        35                  40                  45
Gly Ala Ile Ala Trp Lys Asp Ala His Gly Lys Ala Asp Glu Trp Tyr
    50                  55                  60
Ala Ser Val Glu Ala Leu Arg Ile Ala Asp Asn Val Val Phe Tyr Gln
65                  70                  75                  80
Arg Asp Ser Gly Gly Trp Pro Lys Asn Ile Glu Met Ala Lys Thr Leu
                85                  90                  95
Ser Asp Arg Glu Lys Ala Ala Ile Leu Arg Glu Lys Lys Lys Asn Asp
            100                 105                 110
Ser Thr Ile Asp Asn Gly Ala Thr His Thr Gln Leu Ser Phe Leu Ala
        115                 120                 125
Arg Val Tyr Thr Ala Gln Gln Gln Glu Arg His Arg Glu Ser Phe Leu
    130                 135                 140
Lys Gly Leu Asp Tyr Leu Leu Lys Ala Gln Tyr Ser Asn Gly Gly Trp
145                 150                 155                 160
Pro Gln Phe Tyr Pro Asn Leu Asn Gly Tyr Tyr Lys Arg Ile Thr Tyr
                165                 170                 175
Asn Asp Gly Ala Met Ile Gly Val Met Lys Leu Leu Arg Asp Val Ala
            180                 185                 190
Ala Ala Lys Pro Glu Tyr Ala Phe Val Asp Glu Thr Arg Arg Ala Lys
        195                 200                 205
Ala Ala Asn Ala Val Glu Lys Gly Ile Val Cys Ile Leu Lys Thr Gln
    210                 215                 220
Val Val Val Asp Gly Arg Arg Thr Val Trp Cys Ala Gln His Asp Glu
225                 230                 235                 240
Val Thr Phe Ala Pro Ala Pro Ala Arg Lys Phe Glu Leu Ala Ser Leu
                245                 250                 255
Ser Gly Gly Glu Ser Val Asp Ile Val Arg Phe Leu Met Ser Ile Lys
            260                 265                 270
Asp Pro Ser Arg Asn Val Val Glu Ser Ile Glu Ser Ala Val Lys Trp
        275                 280                 285
Phe Glu Gln Ser Glu Leu Lys Gly Val Lys Trp Val Lys Lys Thr Asp
    290                 295                 300
Ala Thr Gln Pro Asn Gly Phe Asp Cys Val Val Val Lys Asp Pro Glu
305                 310                 315                 320
Ser Ser Val Trp Ala Arg Phe Tyr Glu Ile Gly Thr Asn Arg Pro Ile
                325                 330                 335
Phe Ala Gly Arg Asp Gly Val Pro Lys Tyr Asp Val Ala Gln Ile Glu
            340                 345                 350
His Glu Arg Arg Thr Gly Tyr Glu Trp Tyr Val Asp Glu Ala Ala Lys
        355                 360                 365
Leu Leu Lys Lys Asp Tyr Pro Ala Trp Lys Lys Arg His Val Val Thr
    370                 375                 380
Thr Arg Val His
385
```

<210> 13
<211> 1065
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 13
atgaaaacga tcagccttat ttgcctcgca atctctgctg ggattctgga ttcggttgcg
60
gcggcacgct ggaacgaatt cgcccagaag gcggatgatt ggtatcgagg tgacgaaggc
120
aggcgcgttg cttcgaatat tctttctcac caatcactgc aaggaagctg gcccaagaat
180
accgatacca ccgcgagatt cttcaatgga gatctagcga agattcaggg cacgttcgac
240
aacggtgcga cgacggacga gttgcgtttc ctggcccgcg cgtttgtcgc cacgaaagaa
300
aaaaactacg agtcagcgtt ccgaaaaggc ttcgaacaca ttctcgcggc gcaatacgcg
360
aacggcggat ggccgcaata ttcgccgccg cccaaaagtt accaccgaca cattaccttc
420
aacgataatt cgatggtgcg gctgatgatt ttccttcgcg aggtcacgac ttcgaatctc
480
tactcgttcg tcgaagcgcc gctgcgaaca caagcccgcg aaagtttcga tcgcggtgtg
540
cggtgcattc ttaagtgcca gatcgtcgtg aacgggcaca agaccgcgtg gtgcgcgcaa
600
catgatgaaa cggatttcag cccccgatcc gcgcgtagtt acgaactgcc ttcgctgagc
660
ggttctgaat cagtcggcat tgtgcgcttg ctgatgagcc tcgatcagcc gagccgcgga
720
gtgatcgatg ccatcaccaa cgccgtagcg tggttcgaat cggcgaagct gcccgggatc
780
aaaaccgttc aagagaccga tccgaattcg cccaaaggct ggaatcgcgt cgtcgtaaaa
840
gatgaaagtg cccgaccgat gtgggcgcgt ttctacgaca tcaacaccaa caaaccgttc
900
ttttgtgatc gcgatggtgt gccaaagccg agtcttgccg agatcggtta tgaacggcgg
960
aacggttatg cgtggctcgg atactggcct gaagacttgc tcgcaagaga gtatccagcg
1020
tggaagatga agtggctgaa gcccaaagag cgcccagcat tttga
1065

<210> 14
<211> 354
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(22)

<221> DOMAIN
<222> (23)...(354)
<223> Catalytic domain

<400> 14
Met Lys Thr Ile Ser Leu Ile Cys Leu Ala Ile Ser Ala Gly Ile Leu
 1   5   10   15
Asp Ser Val Ala Ala Ala Arg Trp Asn Glu Phe Ala Gln Lys Ala Asp
            20   25   30
Asp Trp Tyr Arg Gly Asp Glu Gly Arg Arg Val Ala Ser Asn Ile Leu
        35   40   45

Ser His Gln Ser Leu Gln Gly Ser Trp Pro Lys Asn Thr Asp Thr Thr
50 55 60
Ala Arg Phe Phe Asn Gly Asp Leu Ala Lys Ile Gln Gly Thr Phe Asp
65 70 75 80
Asn Gly Ala Thr Thr Asp Glu Leu Arg Phe Leu Ala Arg Ala Phe Val
85 90 95
Ala Thr Lys Glu Lys Asn Tyr Glu Ser Ala Phe Arg Lys Gly Phe Glu
100 105 110
His Ile Leu Ala Ala Gln Tyr Ala Asn Gly Gly Trp Pro Gln Tyr Ser
115 120 125
Pro Pro Pro Lys Ser Tyr His Arg His Ile Thr Phe Asn Asp Asn Ser
130 135 140
Met Val Arg Leu Met Ile Phe Leu Arg Glu Val Thr Thr Ser Asn Leu
145 150 155 160
Tyr Ser Phe Val Glu Ala Pro Leu Arg Thr Gln Ala Arg Glu Ser Phe
165 170 175
Asp Arg Gly Val Arg Cys Ile Leu Lys Cys Gln Ile Val Val Asn Gly
180 185 190
His Lys Thr Ala Trp Cys Ala Gln His Asp Glu Thr Asp Phe Ser Pro
195 200 205
Arg Ser Ala Arg Ser Tyr Glu Leu Pro Ser Leu Ser Gly Ser Glu Ser
210 215 220
Val Gly Ile Val Arg Leu Leu Met Ser Leu Asp Gln Pro Ser Arg Gly
225 230 235 240
Val Ile Asp Ala Ile Thr Asn Ala Val Ala Trp Phe Glu Ser Ala Lys
245 250 255
Leu Pro Gly Ile Lys Thr Val Gln Glu Thr Asp Pro Asn Ser Pro Lys
260 265 270
Gly Trp Asn Arg Val Val Val Lys Asp Glu Ser Ala Arg Pro Met Trp
275 280 285
Ala Arg Phe Tyr Asp Ile Asn Thr Asn Lys Pro Phe Phe Cys Asp Arg
290 295 300
Asp Gly Val Pro Lys Pro Ser Leu Ala Glu Ile Gly Tyr Glu Arg Arg
305 310 315 320
Asn Gly Tyr Ala Trp Leu Gly Tyr Trp Pro Glu Asp Leu Leu Ala Arg
325 330 335
Glu Tyr Pro Ala Trp Lys Met Lys Trp Leu Lys Pro Lys Glu Arg Pro
340 345 350
Ala Phe

<210> 15
<211> 1575
<212> DNA
<213> Bacteria

<400> 15
atgagacgac cagtcgcact ccggctccac gcggcactgg ccaccctggc cctggcggcc
60
gcgaccggcg tggtgctctc gatcccccag gcatcggcgg cggccggcgg cgccaccggc
120
tacgccggcc agaacggcgg caccaccggc ggtgccggcg gccagaccgt acgggccacc
180
acgggcaccg ccatccacgc ggccctgtgc ggacgggcca gcagcagcac cccgatcacg
240
atcgaggtcg agggaacgat caaccacgcc aacaccgcca aggtgtccgg ccccagctgc
300
aacaccgccg ccggagtgat cgagctgaag cagatcagca acgtcacgct cgtcggggtc
360
ggctccggcg ccgtcttcga ccaactcggc atccacatcc gcgagtccag caacatcatc
420

atccagaacg tgacggtccg gaacgtcaag aagtcgggct cgccgctgtc caacggcggc
480
gacgccatcg gcatggagag cgacgtccgc aacgtctggg tcgaccactc caccctggag
540
gcctcgggcg gcgagtccga gggctacgac ggcctcttcg acatgaagga caacacccgg
600
tacgtgaccc tgtcgtacag catcctgcgc aaatccgggc gcggcggcct cgtggggtcc
660
agcgagaccg aactctcgaa cagcttcatc acgtaccacc acaacctgta cgagaacatc
720
gactcgcgcg cgcccctgct gcgcggcggg accgcccaca tgtacaacaa ccactacctg
780
cggatcaacg agtccggcat caactcccgt gccggagccc acgccaaggt ggacaacaac
840
tacttcgagg actccaagga cgtcctcggc accttctaca ccgacgccgc cgggtactgg
900
caggtcagcg gcaacgtcta cgacaacgtg acctggtccg cccggggcac cgacaacaac
960
ccggcggggc cggacccgca gtccaacacc accgtctcca tcccctacgc cttcagcctc
1020
gacccggcca cctgcgtgcc ggacgtcgtg agccgaacgg cgggtgccgg caagggactt
1080
caggtgtcga acggcagctg ctccccgcag acacccacgc ccacgccgac gggcacgccg
1140
accacacccg cgccgacgac tcccaccccg agcccgacgc cctccacgcc cggaccgacc
1200
cagcccggcg ggacgaacct cagcatcggt gccgggtccg acggttcgag caaggccgac
1260
ggcaccagct acggcaacgt ccgggacggg gacctcggca cccactggtc tccggccggt
1320
tcgaccggct ccgtgtcgat caagtggggc agcgccacca cggtctcccg catcgtcatc
1380
cgcgaggcgg cgggcgcgac gggcgtcatc ggctcctggc tcgtcctgaa cggcgacacc
1440
ggcgccgtgc tgacctccgg cagcggggcg gggacgatct ccgtcccccg gacggccctg
1500
aagaagatca ccttcgagat cacgggcgcg agcggcacgc cacggatcgc cgagttcgag
1560
acgtacgccg gctag
1575

<210> 16
<211> 524
<212> PRT
<213> Bacteria

<220>

<221> SIGNAL
<222> (1)...(33)

<221> DOMAIN
<222> (34)...(359)
<223> Catalytic domain

<400> 16
Met Arg Arg Pro Val Ala Leu Arg Leu His Ala Ala Leu Ala Thr Leu
 1   5   10   15
Ala Leu Ala Ala Ala Thr Gly Val Val Leu Ser Ile Pro Gln Ala Ser
            20   25   30
Ala Ala Ala Gly Gly Ala Thr Gly Tyr Ala Gly Gln Asn Gly Gly Thr

```
        35                  40                  45
Thr Gly Gly Ala Gly Gly Gln Thr Val Arg Ala Thr Thr Gly Thr Ala
    50                  55                  60
Ile His Ala Ala Leu Cys Gly Arg Ala Ser Ser Ser Thr Pro Ile Thr
65                  70                  75                  80
Ile Glu Val Glu Gly Thr Ile Asn His Ala Asn Thr Ala Lys Val Ser
                85                  90                  95
Gly Pro Ser Cys Asn Thr Ala Ala Gly Val Ile Glu Leu Lys Gln Ile
            100                 105                 110
Ser Asn Val Thr Leu Val Gly Val Gly Ser Gly Ala Val Phe Asp Gln
        115                 120                 125
Leu Gly Ile His Ile Arg Glu Ser Ser Asn Ile Ile Ile Gln Asn Val
    130                 135                 140
Thr Val Arg Asn Val Lys Lys Ser Gly Ser Pro Leu Ser Asn Gly Gly
145                 150                 155                 160
Asp Ala Ile Gly Met Glu Ser Asp Val Arg Asn Val Trp Val Asp His
                165                 170                 175
Ser Thr Leu Glu Ala Ser Gly Gly Glu Ser Glu Gly Tyr Asp Gly Leu
            180                 185                 190
Phe Asp Met Lys Asp Asn Thr Arg Tyr Val Thr Leu Ser Tyr Ser Ile
        195                 200                 205
Leu Arg Lys Ser Gly Arg Gly Gly Leu Val Gly Ser Ser Glu Thr Glu
    210                 215                 220
Leu Ser Asn Ser Phe Ile Thr Tyr His His Asn Leu Tyr Glu Asn Ile
225                 230                 235                 240
Asp Ser Arg Ala Pro Leu Leu Arg Gly Gly Thr Ala His Met Tyr Asn
                245                 250                 255
Asn His Tyr Leu Arg Ile Asn Glu Ser Gly Ile Asn Ser Arg Ala Gly
            260                 265                 270
Ala His Ala Lys Val Asp Asn Asn Tyr Phe Glu Asp Ser Lys Asp Val
        275                 280                 285
Leu Gly Thr Phe Tyr Thr Asp Ala Ala Gly Tyr Trp Gln Val Ser Gly
    290                 295                 300
Asn Val Tyr Asp Asn Val Thr Trp Ser Ala Arg Gly Thr Asp Asn Asn
305                 310                 315                 320
Pro Ala Gly Pro Asp Pro Gln Ser Asn Thr Thr Val Ser Ile Pro Tyr
                325                 330                 335
Ala Phe Ser Leu Asp Pro Ala Thr Cys Val Pro Asp Val Val Ser Arg
            340                 345                 350
Thr Ala Gly Ala Gly Lys Gly Leu Gln Val Ser Asn Gly Ser Cys Ser
        355                 360                 365
Pro Gln Thr Pro Thr Pro Thr Pro Thr Gly Thr Pro Thr Thr Pro Ala
    370                 375                 380
Pro Thr Thr Pro Thr Pro Ser Pro Thr Pro Ser Thr Pro Gly Pro Thr
385                 390                 395                 400
Gln Pro Gly Gly Thr Asn Leu Ser Ile Gly Ala Gly Ser Asp Gly Ser
                405                 410                 415
Ser Lys Ala Asp Gly Thr Ser Tyr Gly Asn Val Arg Asp Gly Asp Leu
            420                 425                 430
Gly Thr His Trp Ser Pro Ala Gly Ser Thr Gly Ser Val Ser Ile Lys
        435                 440                 445
Trp Gly Ser Ala Thr Thr Val Ser Arg Ile Val Ile Arg Glu Ala Ala
    450                 455                 460
Gly Ala Thr Gly Val Ile Gly Ser Trp Leu Val Leu Asn Gly Asp Thr
465                 470                 475                 480
Gly Ala Val Leu Thr Ser Gly Ser Gly Ala Gly Thr Ile Ser Val Pro
                485                 490                 495
Arg Thr Ala Leu Lys Lys Ile Thr Phe Glu Ile Thr Gly Ala Ser Gly
            500                 505                 510
Thr Pro Arg Ile Ala Glu Phe Glu Thr Tyr Ala Gly
        515                 520
```

<210> 17
<211> 1047
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 17
ttgccgcgtg cgcccggtgg tgagtcgtca tcgccagcgc agacgtcatc ggttgcggtc
60
tcctgggatc agatcctccg tcagcctgcg gcctggtacg gcggtgcgga ggcgttgcga
120
gtcgctgaga acgtgctctt gtatcagcgc gcggcaggag ggtggccgaa gaacatcaac
180
atggcggcgc cgatgaccgc cgctgaccgt gcgaaagtca cggacgagcg cgcgcagaac
240
gacgccacga tcgacaacac gtcaacgacg acgcagatcc gttttcttgc gctcgttctt
300
cgcggcaccg ccgacgcacg attcaaggac gcggcgctga agggcatcga cttcctgctg
360
gctgcgcaat acgcgaatgg aggctggcct cagtattttc ccctgcgcga cgactactcg
420
cggcgcatca cgttcaatga cgacgcgatg gtgaatgtga tgacgctgct gcgcgagact
480
tcgcagggcc agacgccgtt cgagttcgtc gacgcctcgc ggcgcggccg ggcggcgcag
540
tctgtctcac gcggcgtcga cgtcatgctg cgcacgcaga ttcgagtcaa cggcgtgctg
600
accggctggt gccagcagca cgacgagcgg aactttcagc cggtgaaggc gcgcgcgtac
660
gaacatccgt cgattgccag caaggaaacc gcgagcatcg caagattcct gatggggatt
720
gaacggccgt cgccggagat cgtgtccgcg gtggatggcg cagtcgcgtg gttgcgagcg
780
gcgcagattt caggtgtgcg gacggagcgc cggcccgacg gatcgaatcc gggcggcgac
840
gtcgtggcgg tgcaggactc cgccgcgccg ccaatctggg cccgcttcta cgagattggc
900
accaaccggc cgatgttttc gggtcgcgac ggcgtcatca agtacagcct cagcgagatc
960
gagatcgagc ggcgcgctgg atacagctgg tacggcgact acgccgccag actgctcaga
1020
gacgactatc cgaagtggaa gaaatga
1047

<210> 18
<211> 348
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(348)
<223> Catalytic domain

<400> 18
Met Pro Arg Ala Pro Gly Gly Glu Ser Ser Ser Pro Ala Gln Thr Ser

```
 1               5                  10                  15
Ser Val Ala Val Ser Trp Asp Gln Ile Leu Arg Gln Pro Ala Ala Trp
            20                  25                  30
Tyr Gly Gly Ala Glu Ala Leu Arg Val Ala Glu Asn Val Leu Leu Tyr
        35                  40                  45
Gln Arg Ala Ala Gly Gly Trp Pro Lys Asn Ile Asn Met Ala Ala Pro
    50                  55                  60
Met Thr Ala Ala Asp Arg Ala Lys Val Thr Asp Glu Arg Ala Gln Asn
65                  70                  75                  80
Asp Ala Thr Ile Asp Asn Thr Ser Thr Thr Thr Gln Ile Arg Phe Leu
                85                  90                  95
Ala Leu Val Leu Arg Gly Thr Ala Asp Ala Arg Phe Lys Asp Ala Ala
            100                 105                 110
Leu Lys Gly Ile Asp Phe Leu Leu Ala Ala Gln Tyr Ala Asn Gly Gly
        115                 120                 125
Trp Pro Gln Tyr Phe Pro Leu Arg Asp Asp Tyr Ser Arg Arg Ile Thr
    130                 135                 140
Phe Asn Asp Asp Ala Met Val Asn Val Met Thr Leu Leu Arg Glu Thr
145                 150                 155                 160
Ser Gln Gly Gln Thr Pro Phe Glu Phe Val Asp Ala Ser Arg Arg Gly
                165                 170                 175
Arg Ala Ala Gln Ser Val Ser Arg Gly Val Asp Val Met Leu Arg Thr
            180                 185                 190
Gln Ile Arg Val Asn Gly Val Leu Thr Gly Trp Cys Gln Gln His Asp
        195                 200                 205
Glu Arg Asn Phe Gln Pro Val Lys Ala Arg Ala Tyr Glu His Pro Ser
    210                 215                 220
Ile Ala Ser Lys Glu Thr Ala Ser Ile Ala Arg Phe Leu Met Gly Ile
225                 230                 235                 240
Glu Arg Pro Ser Pro Glu Ile Val Ser Ala Val Asp Gly Ala Val Ala
                245                 250                 255
Trp Leu Arg Ala Ala Gln Ile Ser Gly Val Arg Thr Glu Arg Arg Pro
            260                 265                 270
Asp Gly Ser Asn Pro Gly Gly Asp Val Val Ala Val Gln Asp Ser Ala
        275                 280                 285
Ala Pro Pro Ile Trp Ala Arg Phe Tyr Glu Ile Gly Thr Asn Arg Pro
    290                 295                 300
Met Phe Ser Gly Arg Asp Gly Val Ile Lys Tyr Ser Leu Ser Glu Ile
305                 310                 315                 320
Glu Ile Glu Arg Arg Ala Gly Tyr Ser Trp Tyr Gly Asp Tyr Ala Ala
                325                 330                 335
Arg Leu Leu Arg Asp Asp Tyr Pro Lys Trp Lys Lys
            340                 345
```

<210> 19
<211> 1122
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 19
gtgaacaggt ggcgcgaaga cttcttgcgc gacttcgcgg cccgcatgct ccggtgcatg
60
gttccccggc cgcagatcca ctggggcggc ggtgtcatcc ggcaggaacc ggaatggtac
120
ggctcggccg aggcgcgtgc gatcgccgac agcgttcttc aataccagtc gaccgctggc
180
ggctggccca agaacaccga cttgacggtc tcgccaccgt ccgccgaatt ccttgcggat
240

gcggatggtc tcacgaacac gatcgacaac gacgccacca cgttgccgat gcgatttctc
300
gctctggtgg cgcacgcgac cggcggcatc aagtaccgcg ccgcgttcga acgcggtctg
360
gactacctgc tcgccgctca gtatcccaat ggcggctggc ctcagtattt tcccctgcgt
420
gacggctatt actcgcacat cacctacaac gacaatgcga tggtcaacgt cctcaccgtt
480
ctgcgcgatg cggccgcggg ccggcccccc tactcgttcg tcgacagggc ccggcgcgcc
540
agagcagaaa cggccatcgc tcgcggcatc gacatcatcg tgcgcactca ggtgagacgg
600
gccggcgtgc tgaccgcatg gtgcgcccag cacgacgaaa agacgctcga gccggcgtgg
660
gcgcgcaact acgaaccgcc gacactctcc gggcacgaaa gcgtcggcat cgtgcgcttt
720
ctcatgggaa tcgaaaagcc cacgccgagg atcgtcgcgg cggtgcaagg cgccgctgac
780
tggttgagag ccgtcgcgat cagcgggttg cgtctcgagg aattcaccga cgccgatggc
840
aggcgcgaca ggcgcgtcgt cgccgatccg gcagcgccgc tcctgtgggc gcgcttctac
900
gagcttggca cggaccgtcc cgtcttcacc ggccgcgaca aggtgatccg gtactcgctc
960
agcgaaatcg agcacgagcg ccggaacggg tatgcctact atggcacatg gccggccacg
1020
ctcctcagcg aggagtaccc ccgttggcgc gcgaaacacc tggctcgacg gagcgtcagg
1080
caggtagagg agggaatcgc gatacgcgtc cctaatccct ga
1122

<210> 20
<211> 373
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(373)
<223> Catalytic domain

<400> 20
Met Asn Arg Trp Arg Glu Asp Phe Leu Arg Asp Phe Ala Ala Arg Met
 1   5   10   15
Leu Arg Cys Met Val Pro Arg Pro Gln Ile His Trp Gly Gly Gly Val
            20   25   30
Ile Arg Gln Glu Pro Glu Trp Tyr Gly Ser Ala Glu Ala Arg Ala Ile
        35   40   45
Ala Asp Ser Val Leu Gln Tyr Gln Ser Thr Ala Gly Gly Trp Pro Lys
    50   55   60
Asn Thr Asp Leu Thr Val Ser Pro Pro Ser Ala Glu Phe Leu Ala Asp
65   70   75   80
Ala Asp Gly Leu Thr Asn Thr Ile Asp Asn Asp Ala Thr Thr Leu Pro
                85   90   95
Met Arg Phe Leu Ala Leu Val Ala His Ala Thr Gly Gly Ile Lys Tyr
            100   105   110
Arg Ala Ala Phe Glu Arg Gly Leu Asp Tyr Leu Leu Ala Ala Gln Tyr
        115   120   125
Pro Asn Gly Gly Trp Pro Gln Tyr Phe Pro Leu Arg Asp Gly Tyr Tyr

```
    130                 135                 140
Ser His Ile Thr Tyr Asn Asp Asn Ala Met Val Asn Val Leu Thr Val
145                 150                 155                 160
Leu Arg Asp Ala Ala Ala Gly Arg Pro Pro Tyr Ser Phe Val Asp Arg
                165                 170                 175
Ala Arg Arg Ala Arg Ala Glu Thr Ala Ile Ala Arg Gly Ile Asp Ile
            180                 185                 190
Ile Val Arg Thr Gln Val Arg Arg Ala Gly Val Leu Thr Ala Trp Cys
        195                 200                 205
Ala Gln His Asp Glu Lys Thr Leu Glu Pro Ala Trp Ala Arg Asn Tyr
    210                 215                 220
Glu Pro Pro Thr Leu Ser Gly His Glu Ser Val Gly Ile Val Arg Phe
225                 230                 235                 240
Leu Met Gly Ile Glu Lys Pro Thr Pro Arg Ile Val Ala Ala Val Gln
                245                 250                 255
Gly Ala Ala Asp Trp Leu Arg Ala Val Ala Ile Ser Gly Leu Arg Leu
            260                 265                 270
Glu Glu Phe Thr Asp Ala Asp Gly Arg Arg Asp Arg Arg Val Val Ala
        275                 280                 285
Asp Pro Ala Ala Pro Leu Leu Trp Ala Arg Phe Tyr Glu Leu Gly Thr
    290                 295                 300
Asp Arg Pro Val Phe Thr Gly Arg Asp Lys Val Ile Arg Tyr Ser Leu
305                 310                 315                 320
Ser Glu Ile Glu His Glu Arg Arg Asn Gly Tyr Ala Tyr Tyr Gly Thr
                325                 330                 335
Trp Pro Ala Thr Leu Leu Ser Glu Glu Tyr Pro Arg Trp Arg Ala Lys
            340                 345                 350
His Leu Ala Arg Arg Ser Val Arg Gln Val Glu Glu Gly Ile Ala Ile
        355                 360                 365
Arg Val Pro Asn Pro
    370
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<210> 21
<211> 1269
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 21
atgcgtaaat cgaactgggc cgtcacaacg gccatcctgc tcgcgctgag cgccgcaccg
60
ctggcggcaa agcccatcgg acagatcacc ctcgccgtgc cgctcagccc ggcgcgcctg
120
accgaaacgc cgcctgagca gcgggcgcaa tggcaggcct atctcgccac caccgaggca
180
cagcttaagg cagacaaggc ggcgctggct gccgagcgcg ccggtctggc cgaaatcccc
240
gccaagccga agaccggcag cgccaacacc atgccgctcg acaagccgct ggaatggtac
300
gcgtcgtccg aggcgcgtct ggtcgccgat aatatcgtca gctatcagac tccggcaggc
360
ggctggggca aaaatcaggc ccgcaacgaa cccacgcggt tgaaaggtca ggcctacact
420
atcgatgacg ccgatcccac cggttcgggc aaatggaact tcgtcggcac catcgacaac
480
gacgccacca tcgtggaaat tcgctttctc gcccgcgtag cggcggcggc cacgggcccg
540
gaaggcgacg tctatcgcgc ctccgccacg cgcggcatca cctacttgct ggcggcgcag
600

taccccaatg gcggctggcc gcaggtctgg ccgcttcagg gcggctatca cgacgccatc
660
accctcaatg acggcgcgat gatccatgtg ctcgaactgt ttgacgacat cgccagcgga
720
cagggcgact tcgccttcct gcctgagccg ctgcgcgaca aggtcgaggc cgcacaggca
780
aagggtcaga aggtgcttct cgatcttcag cttaagcgca acggcgaacg caccctgtgg
840
gcgcagcagt acgatccgat taccctcttg cccagcgcgg cgcgtaacta cgagccgtcg
900
tcgatcagca ccggtgaaag cgccggtgtg ctgatctacc tcatgtccct gcccaacccc
960
tcgcctgaag tgcgcgacgc catcgaaaaa ggcgtggccc tgctgatcaa acttcagatc
1020
aacggcatgg catgggaaaa ggacggcatg cgcaaacgtc tggtcgccaa ggctgacgcc
1080
tcgccgctgt ggtcgcgcta tcacgactcg gaaacgctgc tgcccatctt cggtgaccgc
1140
gacatgcgca tcttcgacga cgtcaacgac atcagcgacg aacgcagccg cggctatgcc
1200
tggtatggca caagcccggc acgggccatc gccgaatacg aaaaatggaa acagggcaac
1260
ggcaaatga
1269

<210> 22
<211> 422
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(23)

<221> DOMAIN
<222> (24)...(422)
<223> Catalytic domain

<400> 22
Met Arg Lys Ser Asn Trp Ala Val Thr Thr Ala Ile Leu Leu Ala Leu
 1   5   10   15
Ser Ala Ala Pro Leu Ala Ala Lys Pro Ile Gly Gln Ile Thr Leu Ala
            20   25   30
Val Pro Leu Ser Pro Ala Arg Leu Thr Glu Thr Pro Pro Glu Gln Arg
        35   40   45
Ala Gln Trp Gln Ala Tyr Leu Ala Thr Thr Glu Ala Gln Leu Lys Ala
    50   55   60
Asp Lys Ala Ala Leu Ala Ala Glu Arg Ala Gly Leu Ala Glu Ile Pro
65   70   75   80
Ala Lys Pro Lys Thr Gly Ser Ala Asn Thr Met Pro Leu Asp Lys Pro
                85   90   95
Leu Glu Trp Tyr Ala Ser Ser Glu Ala Arg Leu Val Ala Asp Asn Ile
            100   105   110
Val Ser Tyr Gln Thr Pro Ala Gly Gly Trp Gly Lys Asn Gln Ala Arg
        115   120   125
Asn Glu Pro Thr Arg Leu Lys Gly Gln Ala Tyr Thr Ile Asp Asp Ala
    130   135   140
Asp Pro Thr Gly Ser Gly Lys Trp Asn Phe Val Gly Thr Ile Asp Asn
145   150   155   160

Asp Ala Thr Ile Val Glu Ile Arg Phe Leu Ala Arg Val Ala Ala Ala
165 170 175
Ala Thr Gly Pro Glu Gly Asp Val Tyr Arg Ala Ser Ala Thr Arg Gly
180 185 190
Ile Thr Tyr Leu Leu Ala Ala Gln Tyr Pro Asn Gly Gly Trp Pro Gln
195 200 205
Val Trp Pro Leu Gln Gly Gly Tyr His Asp Ala Ile Thr Leu Asn Asp
210 215 220
Gly Ala Met Ile His Val Leu Glu Leu Phe Asp Asp Ile Ala Ser Gly
225 230 235 240
Gln Gly Asp Phe Ala Phe Leu Pro Glu Pro Leu Arg Asp Lys Val Glu
245 250 255
Ala Ala Gln Ala Lys Gly Gln Lys Val Leu Leu Asp Leu Gln Leu Lys
260 265 270
Arg Asn Gly Glu Arg Thr Leu Trp Ala Gln Gln Tyr Asp Pro Ile Thr
275 280 285
Leu Leu Pro Ser Ala Ala Arg Asn Tyr Glu Pro Ser Ser Ile Ser Thr
290 295 300
Gly Glu Ser Ala Gly Val Leu Ile Tyr Leu Met Ser Leu Pro Asn Pro
305 310 315 320
Ser Pro Glu Val Arg Asp Ala Ile Glu Lys Gly Val Ala Leu Leu Ile
325 330 335
Lys Leu Gln Ile Asn Gly Met Ala Trp Glu Lys Asp Gly Met Arg Lys
340 345 350
Arg Leu Val Ala Lys Ala Asp Ala Ser Pro Leu Trp Ser Arg Tyr His
355 360 365
Asp Ser Glu Thr Leu Leu Pro Ile Phe Gly Asp Arg Asp Met Arg Ile
370 375 380
Phe Asp Asp Val Asn Asp Ile Ser Asp Glu Arg Ser Arg Gly Tyr Ala
385 390 395 400
Trp Tyr Gly Thr Ser Pro Ala Arg Ala Ile Ala Glu Tyr Glu Lys Trp
405 410 415
Lys Gln Gly Asn Gly Lys
420

<210> 23
<211> 1182
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 23
atgaaccgtg gcgtgattgt tttgctggcg gccgctccag ctgcggcgca tggcgcagtg
60
ctggggtata tgacgcctgc gcagccgttg accgaggcgc gcattgccgc gctgccggcg
120
tcggagcagg gcgcctggcg gggctacctc gcccgctccc gcgcagccat ggacgccgac
180
aaggccgccc tggccgccga gcgcgccgcg ctcgccaccg taccgccggc gccgccgcat
240
ggcggtggtg atggcgggat ggcgcgcaac cgtccgacgg cttggtatgg gacgccggaa
300
gcgcggcaca tcgcggacaa tatcgtcagc ttccagacgc cgtccggcgg ctggggcaag
360
aacgtggacc gcacgggacc tgtgcgccag cgcggacagc attacgtttc cttcgatggc
420
aaggagtcct ggaacttcat cggcacgatc gacaacaacg ccacaacgag cgagctgaaa
480
ttcctggcgc gcgtgcaggc gcaaatgccc ggcgcggcgg gcgacgaata ccggaaggcc

540
gccctgcgcg gcatcagcta cctgttgaac tcacaatatc ccaacggcgg cttcccgcag
600
gtctatccgc tgcaaggcgg ctaccacgac gccatcacct tcaacgacga tgccttcgcc
660
aacgtgctgc aagtgctgct ggaagtggcg aaccgcaggg gcgactatgc cttcgtcccc
720
gaaaccgtgg caaccgatgc ccgcgcggcc gcggacaagg cgctccaagt cctgctggcg
780
agccagatca tcgtcggcgg cgtacgcacc gcctggtgcc agcagcacga tgcgatcacg
840
ctggcgcccg tcggcgcccg caatttcgaa ccggccgcgc tgaccagcac ggaaagcgcg
900
cgcctgctga tgctgttgat gctgctgccc gatccgagcc cggagctgag agcgtcaatc
960
catgcgggga tggcctggct gcagaaagcg gcgctgccgg gggatgtctg gtcgcgctac
1020
tatgacctga acacgatgag gccgatcttt ggggatcgtg accgcagtat ccacgatgat
1080
gtgaaggaat tgagcgagga gaggcaaaaa ggctatggct ggttcagtaa cggaccagcc
1140
agagctaaac aggcttttga ggcctggacg cgcaaacctt ga
1182

<210> 24
<211> 393
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(18)

<221> DOMAIN
<222> (19)...(393)
<223> Catalytic domain

<400> 24
Met Asn Arg Gly Val Ile Val Leu Leu Ala Ala Ala Pro Ala Ala Ala
 1   5   10   15
His Gly Ala Val Leu Gly Tyr Met Thr Pro Ala Gln Pro Leu Thr Glu
            20   25   30
Ala Arg Ile Ala Ala Leu Pro Ala Ser Glu Gln Gly Ala Trp Arg Gly
        35   40   45
Tyr Leu Ala Arg Ser Arg Ala Ala Met Asp Ala Asp Lys Ala Ala Leu
    50   55   60
Ala Ala Glu Arg Ala Ala Leu Ala Thr Val Pro Pro Ala Pro Pro His
65   70   75   80
Gly Gly Gly Asp Gly Gly Met Ala Arg Asn Arg Pro Thr Ala Trp Tyr
                85   90   95
Gly Thr Pro Glu Ala Arg His Ile Ala Asp Asn Ile Val Ser Phe Gln
            100   105   110
Thr Pro Ser Gly Gly Trp Gly Lys Asn Val Asp Arg Thr Gly Pro Val
        115   120   125
Arg Gln Arg Gly Gln His Tyr Val Ser Phe Asp Gly Lys Glu Ser Trp
    130   135   140
Asn Phe Ile Gly Thr Ile Asp Asn Asn Ala Thr Thr Ser Glu Leu Lys
145   150   155   160
Phe Leu Ala Arg Val Gln Ala Gln Met Pro Gly Ala Ala Gly Asp Glu

```
                165                 170                 175
Tyr Arg Lys Ala Ala Leu Arg Gly Ile Ser Tyr Leu Leu Asn Ser Gln
            180                 185                 190
Tyr Pro Asn Gly Gly Phe Pro Gln Val Tyr Pro Leu Gln Gly Gly Tyr
        195                 200                 205
His Asp Ala Ile Thr Phe Asn Asp Asp Ala Phe Ala Asn Val Leu Gln
    210                 215                 220
Val Leu Leu Glu Val Ala Asn Arg Arg Gly Asp Tyr Ala Phe Val Pro
225                 230                 235                 240
Glu Thr Val Ala Thr Asp Ala Arg Ala Ala Ala Asp Lys Ala Leu Gln
                245                 250                 255
Val Leu Leu Ala Ser Gln Ile Ile Val Gly Gly Val Arg Thr Ala Trp
            260                 265                 270
Cys Gln Gln His Asp Ala Ile Thr Leu Ala Pro Val Gly Ala Arg Asn
        275                 280                 285
Phe Glu Pro Ala Ala Leu Thr Ser Thr Glu Ser Ala Arg Leu Leu Met
    290                 295                 300
Leu Leu Met Leu Leu Pro Asp Pro Ser Pro Glu Leu Arg Ala Ser Ile
305                 310                 315                 320
His Ala Gly Met Ala Trp Leu Gln Lys Ala Ala Leu Pro Gly Asp Val
                325                 330                 335
Trp Ser Arg Tyr Tyr Asp Leu Asn Thr Met Arg Pro Ile Phe Gly Asp
            340                 345                 350
Arg Asp Arg Ser Ile His Asp Asp Val Lys Glu Leu Ser Glu Glu Arg
        355                 360                 365
Gln Lys Gly Tyr Gly Trp Phe Ser Asn Gly Pro Ala Arg Ala Lys Gln
    370                 375                 380
Ala Phe Glu Ala Trp Thr Arg Lys Pro
385                 390
```

<210> 25
<211> 1194
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 25
ttggtcgctg ccctattaag ctgcggcagc gccaatctct atgcagaatc aaccgcaaaa
60
tcggttacgc aatcagcagc cacaaatcaa ttgcaaaatg aaaaaagcag ttgggacagc
120
tattacgccg catccaaaaa aatacatcag gcagaccagg attttctcgc cgctgaatta
180
aaaaaactcg gtcagaaaaa accaacattg cccgcacaca ccaaagattt tggttttgat
240
gttaagcagg taaatgcaga ttggtttaaa agtgacgaag gcaaacgtgt gatggagatt
300
attctctcct tccaaacccc gtccggcggt tggtcaaagc gtaccgacat ggccaaggcg
360
gtgcgacaac ctgggcaagc ctttggcgtt gaaaaaggct atatcccaac atttgataat
420
ggcgctacca gcactcaatt gatgttgctc gcgcaagcac accaagccac cggcgatcac
480
cgctttagcg acgcatttgg gcgcggcttg caattaattt tgactgcgca atacccgaat
540
ggtggctggc cacaaaactt tccactaacc ggtagctacc acgattacat cacctacaac
600
gacaatctta cgcgcgacct gatggtagtg ctgcacaaaa cagcgcaggc aaaaaatgat
660

tttgcattcg tgaccaaagc gcagcaaatc gcagcgtcag ctagcctcgc gcgtgcactt
720
gattgcgtat tgaaatcaca agttgtcgtc aatggcacac gcacactctg gggcgcacag
780
cacgatgtta aaacactgca accaaccaaa gcgcgcgcat ttgaaatggt gtcactcact
840
accactgaaa gcgcagccat gctcagtttt ctgatggata tcaaaaatcc cagcgcggat
900
attattcaat ccatacatgc agccatagcc tggtatgagc aaaataaaat cgtcggaaaa
960
acctggacac gtggtgatgc ggaattaaaa gataataaaa attcgcagcc actctgggcg
1020
cgtttttatg agataggcac taataagcct atatttgggg atcgcgatga cactgtgtat
1080
tacgatttgg caaaagtgtc taaagagcgt cgcgaaggtt atgcgtggta ctccactgac
1140
ccgaataaga cgctaaaaaa atatgctgaa tggtctaaaa aatatcccaa ataa
1194

<210> 26
<211> 397
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(15)

<221> DOMAIN
<222> (16)...(397)
<223> Catalytic domain

<400> 26
Met Val Ala Ala Leu Leu Ser Cys Gly Ser Ala Asn Leu Tyr Ala Glu
 1   5   10   15
Ser Thr Ala Lys Ser Val Thr Gln Ser Ala Ala Thr Asn Gln Leu Gln
            20   25   30
Asn Glu Lys Ser Ser Trp Asp Ser Tyr Tyr Ala Ala Ser Lys Lys Ile
        35   40   45
His Gln Ala Asp Gln Asp Phe Leu Ala Ala Glu Leu Lys Lys Leu Gly
    50   55   60
Gln Lys Lys Pro Thr Leu Pro Ala His Thr Lys Asp Phe Gly Phe Asp
65   70   75   80
Val Lys Gln Val Asn Ala Asp Trp Phe Lys Ser Asp Glu Gly Lys Arg
                85   90   95
Val Met Glu Ile Ile Leu Ser Phe Gln Thr Pro Ser Gly Gly Trp Ser
            100   105   110
Lys Arg Thr Asp Met Ala Lys Ala Val Arg Gln Pro Gly Gln Ala Phe
        115   120   125
Gly Val Glu Lys Gly Tyr Ile Pro Thr Phe Asp Asn Gly Ala Thr Ser
    130   135   140
Thr Gln Leu Met Leu Leu Ala Gln Ala His Gln Ala Thr Gly Asp His
145   150   155   160
Arg Phe Ser Asp Ala Phe Gly Arg Gly Leu Gln Leu Ile Leu Thr Ala
                165   170   175
Gln Tyr Pro Asn Gly Gly Trp Pro Gln Asn Phe Pro Leu Thr Gly Ser
            180   185   190
Tyr His Asp Tyr Ile Thr Tyr Asn Asp Asn Leu Thr Arg Asp Leu Met
        195   200   205

Val Val Leu His Lys Thr Ala Gln Ala Lys Asn Asp Phe Ala Phe Val
210 215 220
Thr Lys Ala Gln Gln Ile Ala Ala Ser Ala Ser Leu Ala Arg Ala Leu
225 230 235 240
Asp Cys Val Leu Lys Ser Gln Val Val Val Asn Gly Thr Arg Thr Leu
245 250 255
Trp Gly Ala Gln His Asp Val Lys Thr Leu Gln Pro Thr Lys Ala Arg
260 265 270
Ala Phe Glu Met Val Ser Leu Thr Thr Thr Glu Ser Ala Ala Met Leu
275 280 285
Ser Phe Leu Met Asp Ile Lys Asn Pro Ser Ala Asp Ile Ile Gln Ser
290 295 300
Ile His Ala Ala Ile Ala Trp Tyr Glu Gln Asn Lys Ile Val Gly Lys
305 310 315 320
Thr Trp Thr Arg Gly Asp Ala Glu Leu Lys Asp Asn Lys Asn Ser Gln
325 330 335
Pro Leu Trp Ala Arg Phe Tyr Glu Ile Gly Thr Asn Lys Pro Ile Phe
340 345 350
Gly Asp Arg Asp Asp Thr Val Tyr Tyr Asp Leu Ala Lys Val Ser Lys
355 360 365
Glu Arg Arg Glu Gly Tyr Ala Trp Tyr Ser Thr Asp Pro Asn Lys Thr
370 375 380
Leu Lys Lys Tyr Ala Glu Trp Ser Lys Lys Tyr Pro Lys
385 390 395

<210> 27
<211> 1917
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 27
gtgtctctct ttagaaaact cgcactgccg gttctgtgcg gtctactgct ttctgtcgga
60
gcagaaaccc gagcgtcgaa gcgcattgtc gtggccgctg atggatcggg tgacgtcagg
120
acgattcaac aagcggtgga ccaggttccc aaagacaata cacacccggt cttgattcag
180
atcaagccgg gtgtgtatca ggaacaagtg cgtgtcgccg ccggcaaacg ctttatcact
240
cttcgcggcg acgacgcgag caagaccgtc atcacctatc gattgagcgc actacaagcg
300
ggaaataccc ggttggcatt caccacctta attaatgcag acgactttcg cgccgagaac
360
ctgacgtttg aaaactcctt cggcaccggt tcacaagcgg ttgctttgtt tgtcgatgcg
420
aaccgcgcga cgtttgaaaa ctgccggttc ctcgggtggc aggacacttt gtttgtgaac
480
ggcagccgcc acttcttcaa agactgctac gtcgaaggcc atgtcgattt cattttcggc
540
acggcctccg cagtgtttga gaactgcacc attcacagca aaggcgaagg ttatgtgacc
600
gcgcactatc gcaccagcga tgagatggat accggttttg tctttcatcg ttgtcgtttg
660
accggacgag acacgggccg cggagtttat ctcggaaggc cgtggcgacc ttacgcgcgc
720
gtcgtcttta tcgattgctg gctggacgca cacatcagac ctgaaggctg ggataattgg
780
agagatcctg aacgagagaa gaccgcgtgg tttgccgagt acaagtcaaa agggcccggt

840
gctaatcccg tagctcgtgt cgcgtggtcc aggcagttga cgacagaaca agccgccgag
900
ttttcgcggg aacgcttttt cagccgcgct gttcgcgggc tctctgggca ggccaaccag
960
gcagtcggaa cgatcgcgtg ggacgatgcg cagaaaaaac cgaacgagtg gtatgcgagc
1020
gccgaggcgt tgcgcatcgc cgacaacgtt gttctttatc aacgtgactc cggcggctgg
1080
cccaagaaca tcgacatggg gaagccgctc gacgacaagg gtcgagccgg tcttctgcgc
1140
gtgcgtaaga agaacgattc caccatcgat aacggcgcga cttacacgca actctcgttt
1200
ctagcgcggg tttacacggc gcaaaagcag gagcggcatc gcgagtcgtt tctgaaggga
1260
ctcgattacc tgttgaaggc gcagtatcca aacggaggct ggccgcagtt ctatcccaat
1320
ctcaacggct attacaaaca catcactttc aacgacaacg cgatgatcgg cgtgatgaaa
1380
ctgctgcgcg acgtagcggc agcgaaaccg gcgtatgcgt ttgtcgacga agcacgacga
1440
acgagtgcgg cgaaggcggt cgaaaaagga atcgagtgca tactgaagac gcaggtggtt
1500
gtgaatggcc ggcgcaccgt gtggtgtgcg caacatgacg aagtcacgct cgcgcctgcc
1560
ccggcgagga cgtttgaatt agtttcgctg agtggtggtg aaagcgttga gatcgtgcgc
1620
tttttgatgt cgatcaagaa cccgtcgccg gcggttgtcg aggcgatcga gtcggcggtt
1680
gcgtggttcg agcaatcgca agtgaaagat cccgccggca aacctgcgtg ggcgcgattt
1740
tatgagatcg gcactaatcg tccgatcttc gccgggcgtg acggcgtcgt taagtatgat
1800
gtgaaacaga tcgatgagga acgacgaaag aattacgcat ggtacgttga cgacgcagcg
1860
aaactactga agaccgacta tcctgagtgg aaagaaaaga acgccaaaga tcaatga
1917

<210> 28
<211> 638
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(21)

<221> DOMAIN
<222> (28)...(308)
<223> Pectin methyl esterase domain

<221> DOMAIN
<222> (309)...(638)
<223> Catalytic domain

<400> 28
Met Ser Leu Phe Arg Lys Leu Ala Leu Pro Val Leu Cys Gly Leu Leu
 1   5   10   15
Leu Ser Val Gly Ala Glu Thr Arg Ala Ser Lys Arg Ile Val Val Ala

```
                20                  25                  30
Ala Asp Gly Ser Gly Asp Val Arg Thr Ile Gln Gln Ala Val Asp Gln
            35                  40                  45
Val Pro Lys Asp Asn Thr His Pro Val Leu Ile Gln Ile Lys Pro Gly
    50                  55                  60
Val Tyr Gln Glu Gln Val Arg Val Ala Ala Gly Lys Arg Phe Ile Thr
65                  70                  75                  80
Leu Arg Gly Asp Asp Ala Ser Lys Thr Val Ile Thr Tyr Arg Leu Ser
                85                  90                  95
Ala Leu Gln Ala Gly Asn Thr Arg Leu Ala Phe Thr Thr Leu Ile Asn
            100                 105                 110
Ala Asp Asp Phe Arg Ala Glu Asn Leu Thr Phe Glu Asn Ser Phe Gly
        115                 120                 125
Thr Gly Ser Gln Ala Val Ala Leu Phe Val Asp Ala Asn Arg Ala Thr
    130                 135                 140
Phe Glu Asn Cys Arg Phe Leu Gly Trp Gln Asp Thr Leu Phe Val Asn
145                 150                 155                 160
Gly Ser Arg His Phe Phe Lys Asp Cys Tyr Val Glu Gly His Val Asp
                165                 170                 175
Phe Ile Phe Gly Thr Ala Ser Ala Val Phe Glu Asn Cys Thr Ile His
            180                 185                 190
Ser Lys Gly Glu Gly Tyr Val Thr Ala His Tyr Arg Thr Ser Asp Glu
        195                 200                 205
Met Asp Thr Gly Phe Val Phe His Arg Cys Arg Leu Thr Gly Arg Asp
    210                 215                 220
Thr Gly Arg Gly Val Tyr Leu Gly Arg Pro Trp Arg Pro Tyr Ala Arg
225                 230                 235                 240
Val Val Phe Ile Asp Cys Trp Leu Asp Ala His Ile Arg Pro Glu Gly
                245                 250                 255
Trp Asp Asn Trp Arg Asp Pro Glu Arg Glu Lys Thr Ala Trp Phe Ala
            260                 265                 270
Glu Tyr Lys Ser Lys Gly Pro Gly Ala Asn Pro Val Ala Arg Val Ala
        275                 280                 285
Trp Ser Arg Gln Leu Thr Thr Glu Gln Ala Ala Glu Phe Ser Arg Glu
    290                 295                 300
Arg Phe Phe Ser Arg Ala Val Arg Gly Leu Ser Gly Gln Ala Asn Gln
305                 310                 315                 320
Ala Val Gly Thr Ile Ala Trp Asp Asp Ala Gln Lys Lys Pro Asn Glu
                325                 330                 335
Trp Tyr Ala Ser Ala Glu Ala Leu Arg Ile Ala Asp Asn Val Val Leu
            340                 345                 350
Tyr Gln Arg Asp Ser Gly Gly Trp Pro Lys Asn Ile Asp Met Gly Lys
        355                 360                 365
Pro Leu Asp Asp Lys Gly Arg Ala Gly Leu Leu Arg Val Arg Lys Lys
    370                 375                 380
Asn Asp Ser Thr Ile Asp Asn Gly Ala Thr Tyr Thr Gln Leu Ser Phe
385                 390                 395                 400
Leu Ala Arg Val Tyr Thr Ala Gln Lys Gln Glu Arg His Arg Glu Ser
                405                 410                 415
Phe Leu Lys Gly Leu Asp Tyr Leu Leu Lys Ala Gln Tyr Pro Asn Gly
            420                 425                 430
Gly Trp Pro Gln Phe Tyr Pro Asn Leu Asn Gly Tyr Tyr Lys His Ile
        435                 440                 445
Thr Phe Asn Asp Asn Ala Met Ile Gly Val Met Lys Leu Leu Arg Asp
    450                 455                 460
Val Ala Ala Ala Lys Pro Ala Tyr Ala Phe Val Asp Glu Ala Arg Arg
465                 470                 475                 480
Thr Ser Ala Ala Lys Ala Val Glu Lys Gly Ile Glu Cys Ile Leu Lys
                485                 490                 495
Thr Gln Val Val Val Asn Gly Arg Arg Thr Val Trp Cys Ala Gln His
            500                 505                 510
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Asp Glu Val Thr Leu Ala Pro Ala Pro Ala Arg Thr Phe Glu Leu Val
515 520 525
Ser Leu Ser Gly Gly Glu Ser Val Glu Ile Val Arg Phe Leu Met Ser
530 535 540
Ile Lys Asn Pro Ser Pro Ala Val Val Glu Ala Ile Glu Ser Ala Val
545 550 555 560
Ala Trp Phe Glu Gln Ser Gln Val Lys Asp Pro Ala Gly Lys Pro Ala
565 570 575
Trp Ala Arg Phe Tyr Glu Ile Gly Thr Asn Arg Pro Ile Phe Ala Gly
580 585 590
Arg Asp Gly Val Val Lys Tyr Asp Val Lys Gln Ile Asp Glu Glu Arg
595 600 605
Arg Lys Asn Tyr Ala Trp Tyr Val Asp Asp Ala Ala Lys Leu Leu Lys
610 615 620
Thr Asp Tyr Pro Glu Trp Lys Glu Lys Asn Ala Lys Asp Gln
625 630 635

<210> 29
<211> 1398
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 29
atgattaacc gtcgagattt cataaaagac ctcatcatca cctccgccgg agtcgcggtt
60
ctcccgcaac tggcgttcgg acaaaacgat ccctggaaaa ctcaataccc gcagatcctc
120
gcgcggatca aaccgccgaa atttccgaag cgcgatttcg tcatcacgaa gttcggcgcg
180
aaggcgggaa ccgatagcac gcaagcgatc gctaaagccc tcgacgcttg cgcgaaagcc
240
ggcggcggac gcgtcgtcgt acccgccggc gaatttctca ccggtgcgat ccatctcaag
300
tcgaacacca atctctacgt ctcaaaaggc gcgactctga agttttcgac cgaccccgaa
360
aaatatctgc cgatcgttca cacgcggtgg gaagggatgg agttgatgca tctctcgccg
420
ttcatctacg cgtacgagca gacgaacatc gcgatcaccg gcgagggcac gctcgacggc
480
caaggcaaat cgttcttttg gaagtggcac ggcaacccgc gatacggcgg caaccccgaa
540
gtgatcagtc agcaaaaagc gcgggcgcga ctttacgaga tgatggacaa gaacgtaccc
600
gtcgcggagc gcgtgttcgg tatcgggcac tatctccggc cgcagttcat ccagccgtac
660
aaatgtaaga acgtcttgat cgaaggcgtg acgatcatcg actcgccgat gtgggaagtt
720
catccggtgc tttgcgagaa tgtcaccgtc cgcaatcttc acatctcgtc gcacggtccg
780
aacaacgacg gctgcgatcc cgagtcgtgc aaagacgtcc tgatcgacaa ctgcttcttc
840
gacaccggtg acgactgcat cgcgatcaag tcgggtcgca ataacgacgg tcgtcgtctg
900
aacacaccga ccgagaacat catcgtccgc aactgcacga tgaaagacgg tcacggtggt
960
atcacggtcg gaagcgagat ctcgggcggc gtgcgaaact tgttcgcaca cgattgcaag
1020
atggacagtg cggatctgtg gaccgcgctc cgggtaaaga acaacgcatc gcggggcggc

1080
atgctggaga atttctattt ccgcaacatc accgtcgggc aagtcgcgcg tgctgtggtc
1140
gagatcgatt tcaactatga agaaggcgcg aagggatcgt acacaccggt catgcgcaac
1200
tacgtggtcg aggatctgac gtgcaccagc gggaaccggc ccgtcgatct gcaaggatta
1260
gacaacgcgc caatttacga tgtgtcgctg cgtaacacga ccttcggcgc gatgaagaac
1320
aagagcgtcg tgaagaatgt ccgaggactg aagatcgaaa acgttaccgt cagcggcacg
1380
cgcgtggaga gtttatga
1398

<210> 30
<211> 465
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(27)

<221> DOMAIN
<222> (77)...(459)
<223> Catalytic domain

<400> 30
Met Ile Asn Arg Arg Asp Phe Ile Lys Asp Leu Ile Ile Thr Ser Ala
 1   5   10   15
Gly Val Ala Val Leu Pro Gln Leu Ala Phe Gly Gln Asn Asp Pro Trp
            20   25   30
Lys Thr Gln Tyr Pro Gln Ile Leu Ala Arg Ile Lys Pro Pro Lys Phe
        35   40   45
Pro Lys Arg Asp Phe Val Ile Thr Lys Phe Gly Ala Lys Ala Gly Thr
    50   55   60
Asp Ser Thr Gln Ala Ile Ala Lys Ala Leu Asp Ala Cys Ala Lys Ala
65   70   75   80
Gly Gly Gly Arg Val Val Val Pro Ala Gly Glu Phe Leu Thr Gly Ala
                85   90   95
Ile His Leu Lys Ser Asn Thr Asn Leu Tyr Val Ser Lys Gly Ala Thr
            100   105   110
Leu Lys Phe Ser Thr Asp Pro Glu Lys Tyr Leu Pro Ile Val His Thr
        115   120   125
Arg Trp Glu Gly Met Glu Leu Met His Leu Ser Pro Phe Ile Tyr Ala
    130   135   140
Tyr Glu Gln Thr Asn Ile Ala Ile Thr Gly Glu Gly Thr Leu Asp Gly
145   150   155   160
Gln Gly Lys Ser Phe Phe Trp Lys Trp His Gly Asn Pro Arg Tyr Gly
                165   170   175
Gly Asn Pro Glu Val Ile Ser Gln Gln Lys Ala Arg Ala Arg Leu Tyr
            180   185   190
Glu Met Met Asp Lys Asn Val Pro Val Ala Glu Arg Val Phe Gly Ile
        195   200   205
Gly His Tyr Leu Arg Pro Gln Phe Ile Gln Pro Tyr Lys Cys Lys Asn
    210   215   220
Val Leu Ile Glu Gly Val Thr Ile Ile Asp Ser Pro Met Trp Glu Val
225   230   235   240
His Pro Val Leu Cys Glu Asn Val Thr Val Arg Asn Leu His Ile Ser

```
                245                 250                 255
Ser His Gly Pro Asn Asn Asp Gly Cys Asp Pro Glu Ser Cys Lys Asp
            260                 265                 270
Val Leu Ile Asp Asn Cys Phe Phe Asp Thr Gly Asp Asp Cys Ile Ala
        275                 280                 285
Ile Lys Ser Gly Arg Asn Asn Asp Gly Arg Arg Leu Asn Thr Pro Thr
    290                 295                 300
Glu Asn Ile Ile Val Arg Asn Cys Thr Met Lys Asp Gly His Gly Gly
305                 310                 315                 320
Ile Thr Val Gly Ser Glu Ile Ser Gly Gly Val Arg Asn Leu Phe Ala
                325                 330                 335
His Asp Cys Lys Met Asp Ser Ala Asp Leu Trp Thr Ala Leu Arg Val
            340                 345                 350
Lys Asn Asn Ala Ser Arg Gly Gly Met Leu Glu Asn Phe Tyr Phe Arg
        355                 360                 365
Asn Ile Thr Val Gly Gln Val Ala Arg Ala Val Val Glu Ile Asp Phe
    370                 375                 380
Asn Tyr Glu Glu Gly Ala Lys Gly Ser Tyr Thr Pro Val Met Arg Asn
385                 390                 395                 400
Tyr Val Val Glu Asp Leu Thr Cys Thr Ser Gly Asn Arg Pro Val Asp
                405                 410                 415
Leu Gln Gly Leu Asp Asn Ala Pro Ile Tyr Asp Val Ser Leu Arg Asn
            420                 425                 430
Thr Thr Phe Gly Ala Met Lys Asn Lys Ser Val Val Lys Asn Val Arg
        435                 440                 445
Gly Leu Lys Ile Glu Asn Val Thr Val Ser Gly Thr Arg Val Glu Ser
    450                 455                 460
Leu
465
```

<210> 31
<211> 1401
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 31
atgatcaatc tttatggcgt ctttgacatc cggacctttg gggcccaacc ggacggagaa
60
acgccttcca ctgcggcgat tacggcggcc atcgaaactt gtgccgcggc cgggggagga
120
gtggtctaca tcccggccgg acggttcctc accggtcccc tccgcctcaa aagccacgtc
180
cggctccatc tcgaggccgg agcgcacttg ctctttagtc aggacccggc cgattatcct
240
gttctggaga cgaggtggga ggggaaggag gtcttgacct atgcacacca gatctacggc
300
gaggacctcg aaggggtcgc gattaccggt cgggggacca tcgacggccg gggcgagact
360
tggtggcgac tcttccgcgc caaagccttc acccatcccc gaccccgcct catcgccttt
420
acccgctgca aggacatcct gatagaagga gtaaccctcg tcaattcacc ggcctggacc
480
atcaatcctg tgatgtgcga gcgggtgacc atcgataagg tgactatcat caacccgccc
540
gactcgccca acaccgacgg gatcgacccc gattcctccc ggaacgtcta tatcactaac
600
tgctacattg acgtaggcga tgactgcatc gccatcaaag cgggccgaga ggactccctt
660

tatcggacgc cttgtgaaaa cattgtcatc gccaactgcc tcatgcgcca cggtcacggc
720
ggggtggtca tcggcagcga gaccagcggg ggtattcgca aggtagtcat taccaactgc
780
atcttcgagg acaccgaccg gggcattaga cttaagtccc ggcgcggacg cggcgggttc
840
gtcgaggacc tccgggcgac gaatattatc atggaaaagg tgctctgtcc cttcgtcctc
900
aacatgtact atgataccgg gggaggcgtg atcgacgagc gcgcgcatga cttagaaccc
960
catccggtaa gcgaggctac accctccttc cgccgcctct ccttcagtca cattactgcc
1020
cgggaagtgc aggccgccgc ggccttcctc tacggcctgc ccgaacagcc tctggaggac
1080
gtcttatttg acgatatctg gatagagctg gccgccgacg cttctcctgc ccgtccggcc
1140
atgatgcggg ccgtcccgcc catgagccaa ggtggtgtgc tctgctacgg tgcgcggcgg
1200
atctccttcc ggcacatgca cctccgcggg caccgcggtc cggccttcca gatcgaacgc
1260
gcggaggcgg tgcagttgat gggctgctcg accgacggca gtgaagaccc ccagcttgtc
1320
ttgggtcaag cggaggaggt caccatccgt gactgcacct ttaccgccca gcaggacccc
1380
gcaaaagaaa ggcaaaatta a
1401

<210> 32
<211> 466
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(348)
<223> Catalytic domain

<400> 32
Met Ile Asn Leu Tyr Gly Val Phe Asp Ile Arg Thr Phe Gly Ala Gln
 1   5   10   15
Pro Asp Gly Glu Thr Pro Ser Thr Ala Ala Ile Thr Ala Ala Ile Glu
            20   25   30
Thr Cys Ala Ala Ala Gly Gly Gly Val Val Tyr Ile Pro Ala Gly Arg
        35   40   45
Phe Leu Thr Gly Pro Leu Arg Leu Lys Ser His Val Arg Leu His Leu
    50   55   60
Glu Ala Gly Ala His Leu Leu Phe Ser Gln Asp Pro Ala Asp Tyr Pro
65   70   75   80
Val Leu Glu Thr Arg Trp Glu Gly Lys Glu Val Leu Thr Tyr Ala His
                85   90   95
Gln Ile Tyr Gly Glu Asp Leu Glu Gly Val Ala Ile Thr Gly Arg Gly
            100   105   110
Thr Ile Asp Gly Arg Gly Glu Thr Trp Trp Arg Leu Phe Arg Ala Lys
        115   120   125
Ala Phe Thr His Pro Arg Pro Arg Leu Ile Ala Phe Thr Arg Cys Lys
    130   135   140
Asp Ile Leu Ile Glu Gly Val Thr Leu Val Asn Ser Pro Ala Trp Thr
145   150   155   160
Ile Asn Pro Val Met Cys Glu Arg Val Thr Ile Asp Lys Val Thr Ile

```
                165                 170                 175
Ile Asn Pro Pro Asp Ser Pro Asn Thr Asp Gly Ile Asp Pro Asp Ser
            180                 185                 190
Ser Arg Asn Val Tyr Ile Thr Asn Cys Tyr Ile Asp Val Gly Asp Asp
        195                 200                 205
Cys Ile Ala Ile Lys Ala Gly Arg Glu Asp Ser Leu Tyr Arg Thr Pro
    210                 215                 220
Cys Glu Asn Ile Val Ile Ala Asn Cys Leu Met Arg His Gly His Gly
225                 230                 235                 240
Gly Val Val Ile Gly Ser Glu Thr Ser Gly Gly Ile Arg Lys Val Val
                245                 250                 255
Ile Thr Asn Cys Ile Phe Glu Asp Thr Asp Arg Gly Ile Arg Leu Lys
            260                 265                 270
Ser Arg Arg Gly Arg Gly Gly Phe Val Glu Asp Leu Arg Ala Thr Asn
        275                 280                 285
Ile Ile Met Glu Lys Val Leu Cys Pro Phe Val Leu Asn Met Tyr Tyr
    290                 295                 300
Asp Thr Gly Gly Gly Val Ile Asp Glu Arg Ala His Asp Leu Glu Pro
305                 310                 315                 320
His Pro Val Ser Glu Ala Thr Pro Ser Phe Arg Arg Leu Ser Phe Ser
                325                 330                 335
His Ile Thr Ala Arg Glu Val Gln Ala Ala Ala Ala Phe Leu Tyr Gly
            340                 345                 350
Leu Pro Glu Gln Pro Leu Glu Asp Val Leu Phe Asp Asp Ile Trp Ile
        355                 360                 365
Glu Leu Ala Ala Asp Ala Ser Pro Ala Arg Pro Ala Met Met Arg Ala
    370                 375                 380
Val Pro Pro Met Ser Gln Gly Gly Val Leu Cys Tyr Gly Ala Arg Arg
385                 390                 395                 400
Ile Ser Phe Arg His Met His Leu Arg Gly His Arg Gly Pro Ala Phe
                405                 410                 415
Gln Ile Glu Arg Ala Glu Ala Val Gln Leu Met Gly Cys Ser Thr Asp
            420                 425                 430
Gly Ser Glu Asp Pro Gln Leu Val Leu Gly Gln Ala Glu Glu Val Thr
        435                 440                 445
Ile Arg Asp Cys Thr Phe Thr Ala Gln Gln Asp Pro Ala Lys Glu Arg
    450                 455                 460
Gln Asn
465
```

<210> 33
<211> 1041
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 33
atgaaacttc gatgtctgat gctcaccctg cttctttgcg gcagcgcctt cgccgccgac
60
cggattacgg ccgacaagat caacaacaag cccgactcct ggcttaccag cgacgaaggc
120
atcaagctga tcgacaacat catcacctgg cagaaccccg agggtggctg ggccaagtac
180
tacgacgcga ccaatccgca caaacaaggc gaagtctacg gcgactggga cggcgtcggc
240
accatcgaca acggctacac ctacaccgag ctgaatctcc tggcgcacgt ctacaccctc
300
accaagcgcc cggagatcct cgattcgttc aacaagggcc tggagtttct gctcaaagcc
360

caatacccca gcggcggctg gccgcaacgg tttccggtgc ccaacaacta cggcaagtgc
420
atcacgctca acgacaacgc gatggtgaac gtgatgcagt tcctgcagaa cgtcgcaaag
480
ggcaaggaag acttcgcttt cgtcgacgag cagcgtcgcg ccaaagcgaa ggaggcgttt
540
gaccgcggga tcgactgcct tctgaagctc cagattaccg tgaacggcaa gcttaccgcc
600
tgggcccagc agtatgaccc gaagacactc gccgcggcgc ccgcccgggc gtacgagctc
660
ccgggcctca gcggctgcga aagcgcgccc gtcatgcgct tgttcatgtc tttggagaac
720
cccagtcccg aagttcagcg cgccgtccac gcggcggcgg cttggtacga ggcgtcgaag
780
atcaccggca agaagctggt gcgcgagaac aacgacgtga cactggccga cgaccccaac
840
ggcgagccgc tttgggcgcg cttctacgac atcgaaacca accgcccgtt ctattgcggt
900
cgcgacggcg tgaagaagtg gtcgctggac gagatcgagc ccgaacgccg caagggctac
960
gcttgggtcc gcccctgggc gacgagcgta ctggagcagt atcgcaagtg ggcggcgaag
1020
cacccacccg tgaacagttg a
1041

<210> 34
<211> 346
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(18)

<221> DOMAIN
<222> (19)...(346)
<223> Catalytic domain

<400> 34
Met Lys Leu Arg Cys Leu Met Leu Thr Leu Leu Leu Cys Gly Ser Ala
 1   5   10   15
Phe Ala Ala Asp Arg Ile Thr Ala Asp Lys Ile Asn Asn Lys Pro Asp
            20   25   30
Ser Trp Leu Thr Ser Asp Glu Gly Ile Lys Leu Ile Asp Asn Ile Ile
        35   40   45
Thr Trp Gln Asn Pro Glu Gly Gly Trp Ala Lys Tyr Tyr Asp Ala Thr
    50   55   60
Asn Pro His Lys Gln Gly Glu Val Tyr Gly Asp Trp Asp Gly Val Gly
65   70   75   80
Thr Ile Asp Asn Gly Tyr Thr Tyr Thr Glu Leu Asn Leu Leu Ala His
                85   90   95
Val Tyr Thr Leu Thr Lys Arg Pro Glu Ile Leu Asp Ser Phe Asn Lys
            100   105   110
Gly Leu Glu Phe Leu Leu Lys Ala Gln Tyr Pro Ser Gly Gly Trp Pro
        115   120   125
Gln Arg Phe Pro Val Pro Asn Asn Tyr Gly Lys Cys Ile Thr Leu Asn
    130   135   140
Asp Asn Ala Met Val Asn Val Met Gln Phe Leu Gln Asn Val Ala Lys
145   150   155   160

Gly Lys Glu Asp Phe Ala Phe Val Asp Glu Gln Arg Arg Ala Lys Ala
165 170 175
Lys Glu Ala Phe Asp Arg Gly Ile Asp Cys Leu Leu Lys Leu Gln Ile
180 185 190
Thr Val Asn Gly Lys Leu Thr Ala Trp Ala Gln Gln Tyr Asp Pro Lys
195 200 205
Thr Leu Ala Ala Ala Pro Ala Arg Ala Tyr Glu Leu Pro Gly Leu Ser
210 215 220
Gly Cys Glu Ser Ala Pro Val Met Arg Leu Phe Met Ser Leu Glu Asn
225 230 235 240
Pro Ser Pro Glu Val Gln Arg Ala Val His Ala Ala Ala Ala Trp Tyr
245 250 255
Glu Ala Ser Lys Ile Thr Gly Lys Lys Leu Val Arg Glu Asn Asn Asp
260 265 270
Val Thr Leu Ala Asp Asp Pro Asn Gly Glu Pro Leu Trp Ala Arg Phe
275 280 285
Tyr Asp Ile Glu Thr Asn Arg Pro Phe Tyr Cys Gly Arg Asp Gly Val
290 295 300
Lys Lys Trp Ser Leu Asp Glu Ile Glu Pro Glu Arg Arg Lys Gly Tyr
305 310 315 320
Ala Trp Val Arg Pro Trp Ala Thr Ser Val Leu Glu Gln Tyr Arg Lys
325 330 335
Trp Ala Ala Lys His Pro Pro Val Asn Ser
340 345

<210> 35
<211> 1071
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 35
atgccaaaaa attccgacga cgcgtggcgg gaaaagactc cgcccgattg gagtcttgtc
60
acatggagcg acgtattcaa acagaagcct ctctggtacc aaaccgacga ggcggctcga
120
gtcgcggacc aactcctcat ctatcaaaaa gagaacggcg ggtttgagaa gaatgtcgac
180
atggcgttga tgctgacgca gaaggaaaaa gaagagctca ccgcaaagcg gtcagacgtc
240
tccgaaacga cgatcgacaa ccggaccacg tatcctcagg tcgcgtatct cggtcgagta
300
atcaccgcaa gccttcttaa accttcgccg ccggcgaatc ttccgaaata caaagacgcc
360
ttcaacaaag gtcttgatta cctgcttgcc tcccagtatg agaacggagg atttccgcaa
420
ttctatccgt tgaaaaaagg ctattacaca cacatcacct tcaacgacga cgcgatgatc
480
ggcgtcctga aggtgcttcg cgacatcgca aataagaaag aggattacgt gttcgtggat
540
gaagcgcgaa gacttcgcgc cgagcaagcg gtcgccaaag cgctgcctct tattctgaag
600
cttcaggttg tcgtcgacgg aaagaaaacc gtctgggctg cgcagtatga cgagactacg
660
ctggcgcctg cagcggctcg caagtttgag cccgtgtcgt tgaccgctgg tgagagcgtc
720
ggcatcgtcc gatacctgat gcaggaaaaa ccgacgccgg agatcaccga tgcgatcgag
780
tctgcgatcg attggtatcg aaagaacaag atcgacggaa tacgttggga gcgcatcaaa

840
ggcgagaaca cggttgtgaa agacaaatcg gctcccccta tatgggcacg gttctatcag
900
atcgaaacga tgcgtccgat cttcatcgga cgtgattcgg ttatcaagta tgacgtgacg
960
caggtcgaag ccgagcgtcg gaatggttac gcctggtacg tcaccgcacc gaatgaattg
1020
gtgaacgagg attatttgaa gtggaagggg aaaagcgccg gagccaagta g
1071

<210> 36
<211> 356
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(356)
<223> Catalytic domain

<400> 36
Met Pro Lys Asn Ser Asp Asp Ala Trp Arg Glu Lys Thr Pro Pro Asp
 1   5   10   15
Trp Ser Leu Val Thr Trp Ser Asp Val Phe Lys Gln Lys Pro Leu Trp
            20   25   30
Tyr Gln Thr Asp Glu Ala Ala Arg Val Ala Asp Gln Leu Leu Ile Tyr
        35   40   45
Gln Lys Glu Asn Gly Gly Phe Glu Lys Asn Val Asp Met Ala Leu Met
    50   55   60
Leu Thr Gln Lys Glu Lys Glu Glu Leu Thr Ala Lys Arg Ser Asp Val
65   70   75   80
Ser Glu Thr Thr Ile Asp Asn Arg Thr Thr Tyr Pro Gln Val Ala Tyr
                85   90   95
Leu Gly Arg Val Ile Thr Ala Ser Leu Leu Lys Pro Ser Pro Pro Ala
            100   105   110
Asn Leu Pro Lys Tyr Lys Asp Ala Phe Asn Lys Gly Leu Asp Tyr Leu
        115   120   125
Leu Ala Ser Gln Tyr Glu Asn Gly Gly Phe Pro Gln Phe Tyr Pro Leu
    130   135   140
Lys Lys Gly Tyr Tyr Thr His Ile Thr Phe Asn Asp Asp Ala Met Ile
145   150   155   160
Gly Val Leu Lys Val Leu Arg Asp Ile Ala Asn Lys Lys Glu Asp Tyr
                165   170   175
Val Phe Val Asp Glu Ala Arg Arg Leu Arg Ala Glu Gln Ala Val Ala
            180   185   190
Lys Ala Leu Pro Leu Ile Leu Lys Leu Gln Val Val Val Asp Gly Lys
        195   200   205
Lys Thr Val Trp Ala Ala Gln Tyr Asp Glu Thr Thr Leu Ala Pro Ala
    210   215   220
Ala Ala Arg Lys Phe Glu Pro Val Ser Leu Thr Ala Gly Glu Ser Val
225   230   235   240
Gly Ile Val Arg Tyr Leu Met Gln Glu Lys Pro Thr Pro Glu Ile Thr
                245   250   255
Asp Ala Ile Glu Ser Ala Ile Asp Trp Tyr Arg Lys Asn Lys Ile Asp
            260   265   270
Gly Ile Arg Trp Glu Arg Ile Lys Gly Glu Asn Thr Val Val Lys Asp
        275   280   285
Lys Ser Ala Pro Pro Ile Trp Ala Arg Phe Tyr Gln Ile Glu Thr Met
    290   295   300

Arg Pro Ile Phe Ile Gly Arg Asp Ser Val Ile Lys Tyr Asp Val Thr
305 310 315 320
Gln Val Glu Ala Glu Arg Arg Asn Gly Tyr Ala Trp Tyr Val Thr Ala
325 330 335
Pro Asn Glu Leu Val Asn Glu Asp Tyr Leu Lys Trp Lys Gly Lys Ser
340 345 350
Ala Gly Ala Lys
355

<210> 37
<211> 1860
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 37
atgttcacta ctactggctc tcattgcgcc cggaattccg cgcgtttttc ccttactgcg
60
atagcagccg ctgttgcgtt gatggcaggc acttcagcat ttgcagctgc gacgggtggc
120
ttctctacca ctgatggtgg caacgtatcg ggcgcccgtt cgtttactgc atcgacttac
180
cagcaaatca acaccattat tgccaacgca aaactggatg atgcaggtaa aaaagtcact
240
gggggtgctt acccgcttat cattacctac accggtaatg aagactcgct gattaaccag
300
atgatcaaag accacacggt gaattcatcg ggcaactgcc ctaacccgcg ttggagcgaa
360
gcctatcgct acgtggaaat taaagagttt accaagggta ttaccattca aggcgcgaat
420
ggttcttcag caaacttcgg cattgtgatt aataaatctg acaatgtgat tgtgcgtaat
480
atgaaaatcg gtgcgcttgc tggtgcgagt aacgatgcgg atatgattcg tatcgacacc
540
ggcgttaacg tgtggattga tcacaacgaa ttgtttgcgg taaataatga atgtaaaggt
600
tcacccgatg gtgacctgac atttgaaagt gcgattgata ttaaaaaagc atcgcaaaat
660
attacggtgt cctacaacat tatccgcgat agtaaaaaag tagggctcga tggttcgagt
720
agcagtgata ttgcaggtgg ccgtaagatt acgttccatc acaatattta tcgcaatgtt
780
ggtgcacgtt taccgttgca acgcggtggt tggacacaca tgtataacaa tctttacgac
840
ggagttacca gctcgggtat taacgttcgt caaggtggct acgcgctaat cgagaacaac
900
tggttccaaa atgctgtcaa cccggttacc tgccgttttg acagtagtaa ctgcggttac
960
tgggatctgc gcaacaacaa cgtgcgcaac cctggtgatt tctccaccta caacattacc
1020
tggaccagcg gtggcaccat cgacgccacc aactggacta ccactcaacc tttcccgatt
1080
agcattcctt acagctactc gcctgttagc ccgcagtgtg tcaaagacaa gttggcaaat
1140
tatgctggtg tcggtaaaaa caatgcgcaa ttaacggcgt ctgcgtgcag cggaaatact
1200
tcatcggtag caccttcatc agtgccagca tcatcggcgg caccttcaag ccgttcatcc
1260
agcagtgcag cgccatccag cacaccaact acatcaagct cgagttcagt tgccgcaacc

1320
ggttcaattt cgctcggtgc aacggcaacc aacaacagca ttgtgttgag ttggtcaccc
1380
aacaatgtga cgctcggttc gcaagaagtg tatcgcgata ccgacgctga tccatcgggg
1440
cgtgtgcgta tcgcatccct ggctgcttca gcgcgtatgt ataccgatag cacagcggca
1500
tcgggccaaa cctattacta ctggattaaa aataccactt ctggtgttgt caccaattcc
1560
aatgctgcat cagcgcgtat tggtagcacg gcgtccagtt ctgttgcatc aagcagctca
1620
agttcaagcg gcggcgcgcc cgtattaggt ggtactggtg attatccaag cggcttctcc
1680
aagtgcgctg atttgggcgg gacttgttca gtgtcatcgg gcgatggctg ggttgcgttt
1740
ggtcgcaaag gcaagtgggt taccaagaaa gtatcggtag gtagttcaat cgcctgtacc
1800
gttgcggcat ttggttcgga tccacagggc aaccctaaca agtgttctta caaacgttaa
1860

<210> 38
<211> 619
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(35)

<221> DOMAIN
<222> (36)...(387)
<223> Catalytic domain

<400> 38
Met Phe Thr Thr Thr Gly Ser His Cys Ala Arg Asn Ser Ala Arg Phe
 1   5   10   15
Ser Leu Thr Ala Ile Ala Ala Ala Val Ala Leu Met Ala Gly Thr Ser
            20   25   30
Ala Phe Ala Ala Ala Thr Gly Gly Phe Ser Thr Thr Asp Gly Gly Asn
        35   40   45
Val Ser Gly Ala Arg Ser Phe Thr Ala Ser Thr Tyr Gln Gln Ile Asn
    50   55   60
Thr Ile Ile Ala Asn Ala Lys Leu Asp Asp Ala Gly Lys Lys Val Thr
65   70   75   80
Gly Gly Ala Tyr Pro Leu Ile Ile Thr Tyr Thr Gly Asn Glu Asp Ser
                85   90   95
Leu Ile Asn Gln Met Ile Lys Asp His Thr Val Asn Ser Ser Gly Asn
            100   105   110
Cys Pro Asn Pro Arg Trp Ser Glu Ala Tyr Arg Tyr Val Glu Ile Lys
        115   120   125
Glu Phe Thr Lys Gly Ile Thr Ile Gln Gly Ala Asn Gly Ser Ser Ala
    130   135   140
Asn Phe Gly Ile Val Ile Asn Lys Ser Asp Asn Val Ile Val Arg Asn
145   150   155   160
Met Lys Ile Gly Ala Leu Ala Gly Ala Ser Asn Asp Ala Asp Met Ile
                165   170   175
Arg Ile Asp Thr Gly Val Asn Val Trp Ile Asp His Asn Glu Leu Phe
            180   185   190
Ala Val Asn Asn Glu Cys Lys Gly Ser Pro Asp Gly Asp Leu Thr Phe

```
        195                 200                 205
Glu Ser Ala Ile Asp Ile Lys Lys Ala Ser Gln Asn Ile Thr Val Ser
    210                 215                 220
Tyr Asn Ile Ile Arg Asp Ser Lys Lys Val Gly Leu Asp Gly Ser Ser
225                 230                 235                 240
Ser Ser Asp Ile Ala Gly Gly Arg Lys Ile Thr Phe His His Asn Ile
                245                 250                 255
Tyr Arg Asn Val Gly Ala Arg Leu Pro Leu Gln Arg Gly Gly Trp Thr
            260                 265                 270
His Met Tyr Asn Asn Leu Tyr Asp Gly Val Thr Ser Ser Gly Ile Asn
        275                 280                 285
Val Arg Gln Gly Gly Tyr Ala Leu Ile Glu Asn Asn Trp Phe Gln Asn
    290                 295                 300
Ala Val Asn Pro Val Thr Cys Arg Phe Asp Ser Ser Asn Cys Gly Tyr
305                 310                 315                 320
Trp Asp Leu Arg Asn Asn Asn Val Arg Asn Pro Gly Asp Phe Ser Thr
                325                 330                 335
Tyr Asn Ile Thr Trp Thr Ser Gly Gly Thr Ile Asp Ala Thr Asn Trp
            340                 345                 350
Thr Thr Thr Gln Pro Phe Pro Ile Ser Ile Pro Tyr Ser Tyr Ser Pro
        355                 360                 365
Val Ser Pro Gln Cys Val Lys Asp Lys Leu Ala Asn Tyr Ala Gly Val
    370                 375                 380
Gly Lys Asn Asn Ala Gln Leu Thr Ala Ser Ala Cys Ser Gly Asn Thr
385                 390                 395                 400
Ser Ser Val Ala Pro Ser Ser Val Pro Ala Ser Ser Ala Ala Pro Ser
                405                 410                 415
Ser Arg Ser Ser Ser Ser Ala Ala Pro Ser Ser Thr Pro Thr Thr Ser
            420                 425                 430
Ser Ser Ser Ser Val Ala Ala Thr Gly Ser Ile Ser Leu Gly Ala Thr
        435                 440                 445
Ala Thr Asn Asn Ser Ile Val Leu Ser Trp Ser Pro Asn Asn Val Thr
    450                 455                 460
Leu Gly Ser Gln Glu Val Tyr Arg Asp Thr Asp Ala Asp Pro Ser Gly
465                 470                 475                 480
Arg Val Arg Ile Ala Ser Leu Ala Ala Ser Ala Arg Met Tyr Thr Asp
                485                 490                 495
Ser Thr Ala Ala Ser Gly Gln Thr Tyr Tyr Tyr Trp Ile Lys Asn Thr
            500                 505                 510
Thr Ser Gly Val Val Thr Asn Ser Asn Ala Ala Ser Ala Arg Ile Gly
        515                 520                 525
Ser Thr Ala Ser Ser Ser Val Ala Ser Ser Ser Ser Ser Ser Ser Gly
    530                 535                 540
Gly Ala Pro Val Leu Gly Gly Thr Gly Asp Tyr Pro Ser Gly Phe Ser
545                 550                 555                 560
Lys Cys Ala Asp Leu Gly Gly Thr Cys Ser Val Ser Ser Gly Asp Gly
                565                 570                 575
Trp Val Ala Phe Gly Arg Lys Gly Lys Trp Val Thr Lys Lys Val Ser
            580                 585                 590
Val Gly Ser Ser Ile Ala Cys Thr Val Ala Ala Phe Gly Ser Asp Pro
        595                 600                 605
Gln Gly Asn Pro Asn Lys Cys Ser Tyr Lys Arg
    610                 615
```

<210> 39
<211> 1077
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 39
atggcgccga tcctccgacc caacctcctt tgcacttacg cgctctgcat gggcttgctc
60
gccgtggtga gctgcgcggc ggggccggtg tcagcgcagc agccggcgcc atggagcacg
120
gccatcgtgg agcaggagga gagcgcgttc gcctccccgt cgatgcgcag cgtcgccgac
180
aacgtcgtgc gccatcagtc ggccgaaggc ggctggccta agaacaccaa tctggcggcg
240
ccgccatcgg ggccggcgcc ggagggcgtc gccaatacga tcgacaatga tgcgacgacg
300
ctgccgatgg agtttctggc gcgtgtgatc cacgccggcg gcgtccgata caagccggcc
360
ttcgagcgcg ggctggatta tctgcttgcg gctcagtacg cgaacggcgg ctggccgcag
420
ttctatccgc tgcgcggggg ctattacgat cacgtgacgt tcaacgacga cgccatgatc
480
cgggtgatga ttctgctcgg cgcagtggcg cgcggcgggg cgccctatga atttgtcgac
540
gccgggcggc gcgcgcgcgc tgcagccgcg gtcgagcggg gcctggcgct catcctgcgc
600
acgcagatcc ggcagggcgg ggcgctgacg gtctggtgcg cgcagtatga cagcgccacc
660
ttgcagcccg cctgggcgcg cgcctatgag ccgccgtccc tgtccggcgc ggaaagtgtg
720
gggatcgtgc gctatctcat gtcgatcgac catccctcgc ccgaagtcgt cgccgccgtc
780
gacggcgctg tggcatggct gcgcgcggcc gccattgccg gcgtgcgcgt ggagaatttc
840
acggacgccg acggccgccc tgaccgccgc gccgtggccg acgcgggcgc gccgccgatc
900
tgggcgcggt tctacgagtt cggcgccaac cggccgatct tcctggggcg tgattccgtt
960
tttcactaca cgttcggaga aatcgagcgc gagcggcgcg caggctacaa ttattacgga
1020
tactgggcgc gctccgtgct ggaagactat ccggcctggc gcgcgcgcgt gcgatga
1077

<210> 40
<211> 358
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(32)

<221> DOMAIN
<222> (33)...(358)
<223> Catalytic domain

<400> 40
Met Ala Pro Ile Leu Arg Pro Asn Leu Leu Cys Thr Tyr Ala Leu Cys
 1   5   10   15
Met Gly Leu Leu Ala Val Val Ser Cys Ala Ala Gly Pro Val Ser Ala
            20   25   30
Gln Gln Pro Ala Pro Trp Ser Thr Ala Ile Val Glu Gln Glu Glu Ser
        35   40   45

Ala Phe Ala Ser Pro Ser Met Arg Ser Val Ala Asp Asn Val Val Arg
50 55 60
His Gln Ser Ala Glu Gly Gly Trp Pro Lys Asn Thr Asn Leu Ala Ala
65 70 75 80
Pro Pro Ser Gly Pro Ala Pro Glu Gly Val Ala Asn Thr Ile Asp Asn
85 90 95
Asp Ala Thr Thr Leu Pro Met Glu Phe Leu Ala Arg Val Ile His Ala
100 105 110
Gly Gly Val Arg Tyr Lys Pro Ala Phe Glu Arg Gly Leu Asp Tyr Leu
115 120 125
Leu Ala Ala Gln Tyr Ala Asn Gly Gly Trp Pro Gln Phe Tyr Pro Leu
130 135 140
Arg Gly Gly Tyr Tyr Asp His Val Thr Phe Asn Asp Asp Ala Met Ile
145 150 155 160
Arg Val Met Ile Leu Leu Gly Ala Val Ala Arg Gly Gly Ala Pro Tyr
165 170 175
Glu Phe Val Asp Ala Gly Arg Arg Ala Arg Ala Ala Ala Ala Val Glu
180 185 190
Arg Gly Leu Ala Leu Ile Leu Arg Thr Gln Ile Arg Gln Gly Gly Ala
195 200 205
Leu Thr Val Trp Cys Ala Gln Tyr Asp Ser Ala Thr Leu Gln Pro Ala
210 215 220
Trp Ala Arg Ala Tyr Glu Pro Pro Ser Leu Ser Gly Ala Glu Ser Val
225 230 235 240
Gly Ile Val Arg Tyr Leu Met Ser Ile Asp His Pro Ser Pro Glu Val
245 250 255
Val Ala Ala Val Asp Gly Ala Val Ala Trp Leu Arg Ala Ala Ala Ile
260 265 270
Ala Gly Val Arg Val Glu Asn Phe Thr Asp Ala Asp Gly Arg Pro Asp
275 280 285
Arg Arg Ala Val Ala Asp Ala Gly Ala Pro Pro Ile Trp Ala Arg Phe
290 295 300
Tyr Glu Phe Gly Ala Asn Arg Pro Ile Phe Leu Gly Arg Asp Ser Val
305 310 315 320
Phe His Tyr Thr Phe Gly Glu Ile Glu Arg Glu Arg Arg Ala Gly Tyr
325 330 335
Asn Tyr Tyr Gly Tyr Trp Ala Arg Ser Val Leu Glu Asp Tyr Pro Ala
340 345 350
Trp Arg Ala Arg Val Arg
355

<210> 41
<211> 1080
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 41
atgaaaaatt taaaatacag tttagtttca tttgtactac tcattactat gaatgttttt
60
acgcaagaaa aaaaagtaac ttggaaaagc atcacagaaa ataacgatga aaattggttt
120
gtaagcgaag aagccaaaaa aatagccgaa aatgttttgt tatatcaacg cgatattggt
180
ggttggccaa aaaacactga attcaaaat gaactttcag aaaaagaaaa actaacatta
240
aaagaattaa aatcggatcc aaaaggatgt accatcgaca atggtgcaac gtgtcaggaa
300
ttacttttct tatccaaaat atataaatcc aatccagatg agcgatataa aatggctttc

360
ttaaaaggtg tgatttacct gattacagct caatacaaaa atggtggttg gccacaatat
420
tacccttga gagaaggata ttacactcat attacttaca acgataatgc aatggtgaat
480
gttttaaagt tgttgaaaga agttaaagat aaatctgatt actactcaat tcaagcaccc
540
gatgaaattt ccaaaatggc tgaagtatca tttaataaag gagtcgattg catattaaaa
600
acacagtaca aacaaaatgg aatattaacc gcttggtgtg cacaacatga cagggaaaca
660
ttgaaacctg ctaaagcaag agcttatgaa ttgccttcgt taagcggaaa agaatcagcc
720
aaaattgtgt tgttattaat gtcaatcgaa aatccatcta aagaagtaat tactgccgta
780
aattcagcag ttaattggtt tgaaaaaaca aaaatcaacg gaattaaaat tgaaaccatt
840
tccaccggga aaaaggatga aaaagataga attgttgttg aaagtcctga tgctccgccg
900
ctttgggcaa gatttatgga attaagtgac aacaaaccat ttttttgtga tcgtgacgga
960
aagaaaaaat acagcatgtc agaaattagt caagagcgta gaaccggcta tgcatggtac
1020
accaacgaac caaaagaagt tttaaaaaaa tacgatgatt ggaagtcatc attaaactaa
1080

<210> 42
<211> 359
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(21)

<221> DOMAIN
<222> (22)...(359)
<223> Catalytic domain

<400> 42
Met Lys Asn Leu Lys Tyr Ser Leu Val Ser Phe Val Leu Leu Ile Thr
 1   5   10   15
Met Asn Val Phe Thr Gln Glu Lys Lys Val Thr Trp Lys Ser Ile Thr
            20   25   30
Glu Asn Asn Asp Glu Asn Trp Phe Val Ser Glu Glu Ala Lys Lys Ile
        35   40   45
Ala Glu Asn Val Leu Leu Tyr Gln Arg Asp Ile Gly Gly Trp Pro Lys
    50   55   60
Asn Thr Glu Ile Gln Asn Glu Leu Ser Glu Lys Glu Lys Leu Thr Leu
65   70   75   80
Lys Glu Leu Lys Ser Asp Pro Lys Gly Cys Thr Ile Asp Asn Gly Ala
                85   90   95
Thr Cys Gln Glu Leu Leu Phe Leu Ser Lys Ile Tyr Lys Ser Asn Pro
            100   105   110
Asp Glu Arg Tyr Lys Met Ala Phe Leu Lys Gly Val Ile Tyr Leu Ile
        115   120   125
Thr Ala Gln Tyr Lys Asn Gly Gly Trp Pro Gln Tyr Tyr Pro Leu Arg
    130   135   140
Glu Gly Tyr Tyr Thr His Ile Thr Tyr Asn Asp Asn Ala Met Val Asn

```
145                 150                 155                 160
Val Leu Lys Leu Leu Lys Glu Val Lys Asp Lys Ser Asp Tyr Tyr Ser
                165                 170                 175
Ile Gln Ala Pro Asp Glu Ile Ser Lys Met Ala Glu Val Ser Phe Asn
            180                 185                 190
Lys Gly Val Asp Cys Ile Leu Lys Thr Gln Tyr Lys Gln Asn Gly Ile
        195                 200                 205
Leu Thr Ala Trp Cys Ala Gln His Asp Arg Glu Thr Leu Lys Pro Ala
    210                 215                 220
Lys Ala Arg Ala Tyr Glu Leu Pro Ser Leu Ser Gly Lys Glu Ser Ala
225                 230                 235                 240
Lys Ile Val Leu Leu Leu Met Ser Ile Glu Asn Pro Ser Lys Glu Val
                245                 250                 255
Ile Thr Ala Val Asn Ser Ala Val Asn Trp Phe Glu Lys Thr Lys Ile
            260                 265                 270
Asn Gly Ile Lys Ile Glu Thr Ile Ser Thr Gly Lys Lys Asp Glu Lys
        275                 280                 285
Asp Arg Ile Val Val Glu Ser Pro Asp Ala Pro Pro Leu Trp Ala Arg
    290                 295                 300
Phe Met Glu Leu Ser Asp Asn Lys Pro Phe Phe Cys Asp Arg Asp Gly
305                 310                 315                 320
Lys Lys Lys Tyr Ser Met Ser Glu Ile Ser Gln Glu Arg Arg Thr Gly
                325                 330                 335
Tyr Ala Trp Tyr Thr Asn Glu Pro Lys Glu Val Leu Lys Lys Tyr Asp
            340                 345                 350
Asp Trp Lys Ser Ser Leu Asn
        355
```

<210> 43
<211> 1902
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 43
gtggatccaa agaattgggg cagcggattt accggcgaaa tcaaagtaac taacaacaca
60
agccaaacag tcaatagctg gtctgtgtca tggcaagagg caggagccag tgtaactaat
120
tcctggaatg caaccttggg agggacgaat ccttataccg caaccgggtt aggatggaac
180
tcaaccctgg cgcccggagc ctctgccagt tttggttttc aagcaaacgg cactgcgggg
240
gcaccaaagg taaatggcag tttgtgtggt gcgactgcat catctgcagc gaccagcaaa
300
tccagtgcga gtgttgcgag ttcaaagatt gcaagttcaa ttcaatcaag tgcaactagc
360
agttcaaaat cgtccagttc tgctgcacct tcaagcacgc caaaatccag tagctctgct
420
ccaacggctg catcattcac tattcaagaa gagcaagccg gtttttgccg tgtagacggt
480
attgcaacgg aaagtaccaa caccggattc accggcaacg gctacaccaa ttccaataat
540
gtacaaggtg ctgccattgt gtgggcggta aatgcaacta ccagtgcacg ccatacaatt
600
actttccgct tcgctaatgg tggcactgcg aatcgcaatg gctcgctagt cattaacggc
660
ggcagcaatg gtaattacac ggtgcaatta ccacgcaccg cgagctgggc tgactggcaa
720
```
```

acagtaagtc tggaaattga tttggtacaa ggcaataaca atttgcaact caccgcattg
780
actgcagatg gcctcgcaaa tatcgacttc atcaaaattg aaggagcatc aaccaaagcg
840
ggaacctgtg caggtgcggt cagcagtagc agtgttgcct cttcggtaaa atccagtgct
900
agcgcggcaa gcagttctgt accaacgaac accggcgcca tgctaacttt ggatggcaac
960
cctgccgcaa gctggcttaa caaatcgcgt acaaagtgga gcgcatcgcg cgctgacatt
1020
gttgcctctt atcaacagtc caacggcggc tggccaaaaa atctggatta caattcagtg
1080
agcgctggta atggcggcag tgcaagcggc accatcgata atggtgcaac tattactgaa
1140
atggtttatc tcgctgaggt ttacaaaacc ggaaacaata ccaagtaccg cgatgcagtt
1200
cgccgtgcag caaactttat cgtgagttcg caatatagca ctggcgcgtt gccgcaattt
1260
tatccgctca aaggtggcta tgcagaccac gccaccttta atgataacgg catggcttac
1320
gcattaactg tattggattt cgctgcaaac aagcgcgcgc cttttgatac ggatgtcttt
1380
aatgacacag accgcgcaaa atttaaaaca gcggtaacca aaggtgttga ttacatttta
1440
aaagcgcaat ggaaacaaaa tggaaaatta acagcctggt gcgcacaaca tggcgcgact
1500
gactatcaac ctaaaaaagc acgcgcttat gaattggaat cactgagtgg tagcgagtct
1560
gttggtgtaa ttgcattttt aatgacgcag ccgcagacag cacaaatcca aacggccgtt
1620
aaagcaggcc tcaactggtt caatagcccg agcacctatt tggaaggtta cacctacgat
1680
tcatccaaag cgtccactaa tcccatagtg cagaaagcgg gaagtagaat gtggtatcgc
1740
ttttacgatt taaataccaa ccgtggtttt ttcagcgacc gggacggcag caaattctat
1800
gacattacca aaatgtctga agaacgtcgc acgggttata gttggggtgg cgcttatggt
1860
gagagcatca tcgcctttgg caaaaaagtg ggctatctat aa
1902

<210> 44
<211> 633
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> BINDING
<222> (4)...(89)
<223> Carbohydrate binding module

<221> BINDING
<222> (152)...(275)
<223> Carbohydrate binding module

<221> DOMAIN
<222> (277)...(633)
<223> Catalytic domain

<400> 44

```
Met Asp Pro Lys Asn Trp Gly Ser Gly Phe Thr Gly Glu Ile Lys Val
 1               5                  10                  15
Thr Asn Asn Thr Ser Gln Thr Val Asn Ser Trp Ser Val Ser Trp Gln
            20                  25                  30
Glu Ala Gly Ala Ser Val Thr Asn Ser Trp Asn Ala Thr Leu Gly Gly
        35                  40                  45
Thr Asn Pro Tyr Thr Ala Thr Gly Leu Gly Trp Asn Ser Thr Leu Ala
    50                  55                  60
Pro Gly Ala Ser Ala Ser Phe Gly Phe Gln Ala Asn Gly Thr Ala Gly
65                  70                  75                  80
Ala Pro Lys Val Asn Gly Ser Leu Cys Gly Ala Thr Ala Ser Ser Ala
                85                  90                  95
Ala Thr Ser Lys Ser Ser Ala Ser Val Ala Ser Ser Lys Ile Ala Ser
            100                 105                 110
Ser Ile Gln Ser Ser Ala Thr Ser Ser Ser Lys Ser Ser Ser Ser Ala
        115                 120                 125
Ala Pro Ser Ser Thr Pro Lys Ser Ser Ser Ser Ala Pro Thr Ala Ala
    130                 135                 140
Ser Phe Thr Ile Gln Glu Glu Gln Ala Gly Phe Cys Arg Val Asp Gly
145                 150                 155                 160
Ile Ala Thr Glu Ser Thr Asn Thr Gly Phe Thr Gly Asn Gly Tyr Thr
                165                 170                 175
Asn Ser Asn Asn Val Gln Gly Ala Ala Ile Val Trp Ala Val Asn Ala
            180                 185                 190
Thr Thr Ser Ala Arg His Thr Ile Thr Phe Arg Phe Ala Asn Gly Gly
        195                 200                 205
Thr Ala Asn Arg Asn Gly Ser Leu Val Ile Asn Gly Gly Ser Asn Gly
    210                 215                 220
Asn Tyr Thr Val Gln Leu Pro Arg Thr Ala Ser Trp Ala Asp Trp Gln
225                 230                 235                 240
Thr Val Ser Leu Glu Ile Asp Leu Val Gln Gly Asn Asn Asn Leu Gln
                245                 250                 255
Leu Thr Ala Leu Thr Ala Asp Gly Leu Ala Asn Ile Asp Phe Ile Lys
            260                 265                 270
Ile Glu Gly Ala Ser Thr Lys Ala Gly Thr Cys Ala Gly Ala Val Ser
        275                 280                 285
Ser Ser Ser Val Ala Ser Ser Val Lys Ser Ser Ala Ser Ala Ala Ser
    290                 295                 300
Ser Ser Val Pro Thr Asn Thr Gly Ala Met Leu Thr Leu Asp Gly Asn
305                 310                 315                 320
Pro Ala Ala Ser Trp Leu Asn Lys Ser Arg Thr Lys Trp Ser Ala Ser
                325                 330                 335
Arg Ala Asp Ile Val Ala Ser Tyr Gln Gln Ser Asn Gly Gly Trp Pro
            340                 345                 350
Lys Asn Leu Asp Tyr Asn Ser Val Ser Ala Gly Asn Gly Gly Ser Ala
        355                 360                 365
Ser Gly Thr Ile Asp Asn Gly Ala Thr Ile Thr Glu Met Val Tyr Leu
    370                 375                 380
Ala Glu Val Tyr Lys Thr Gly Asn Asn Thr Lys Tyr Arg Asp Ala Val
385                 390                 395                 400
Arg Arg Ala Ala Asn Phe Ile Val Ser Ser Gln Tyr Ser Thr Gly Ala
                405                 410                 415
Leu Pro Gln Phe Tyr Pro Leu Lys Gly Gly Tyr Ala Asp His Ala Thr
            420                 425                 430
Phe Asn Asp Asn Gly Met Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala
        435                 440                 445
Ala Asn Lys Arg Ala Pro Phe Asp Thr Asp Val Phe Asn Asp Thr Asp
    450                 455                 460
Arg Ala Lys Phe Lys Thr Ala Val Thr Lys Gly Val Asp Tyr Ile Leu
465                 470                 475                 480
```

Lys Ala Gln Trp Lys Gln Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln
485 490 495
His Gly Ala Thr Asp Tyr Gln Pro Lys Lys Ala Arg Ala Tyr Glu Leu
500 505 510
Glu Ser Leu Ser Gly Ser Glu Ser Val Gly Val Ile Ala Phe Leu Met
515 520 525
Thr Gln Pro Gln Thr Ala Gln Ile Gln Thr Ala Val Lys Ala Gly Leu
530 535 540
Asn Trp Phe Asn Ser Pro Ser Thr Tyr Leu Glu Gly Tyr Thr Tyr Asp
545 550 555 560
Ser Ser Lys Ala Ser Thr Asn Pro Ile Val Gln Lys Ala Gly Ser Arg
565 570 575
Met Trp Tyr Arg Phe Tyr Asp Leu Asn Thr Asn Arg Gly Phe Phe Ser
580 585 590
Asp Arg Asp Gly Ser Lys Phe Tyr Asp Ile Thr Lys Met Ser Glu Glu
595 600 605
Arg Arg Thr Gly Tyr Ser Trp Gly Gly Ala Tyr Gly Glu Ser Ile Ile
610 615 620
Ala Phe Gly Lys Lys Val Gly Tyr Leu
625 630

<210> 45
<211> 987
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 45
atgactagac gcgccttcat cgcggttatc tgtttcttcg cggccgtctg cgcgcacgcg
60
cagtccaccg tgcgctggaa ggacgtgctc gagcagtccg agggctggta ttccacgacc
120
gccgcgcacg tcgtcgccga cacggtgctg ctgtatcaac gtccatccgg tggatggccg
180
aaggacatcg acatgacggc gccgccggcg gaccgcactc ctcccgcgcg tccagacgcg
240
accatcgaca acggcgccac gaccacgcag atccgcctgc tcgctcgtgc ggcctcgggc
300
gcaccggcgg ctgccgccca cacctacacg gcggcggcgc ttcgcgggat cgattacctg
360
ctcgaggcgc agtatcccaa cggcggctgg ccgcagttct tccccctgcg caaggactat
420
tcgcgctacg tcacgttcaa cgacgacgcg atgatgaacg tgatgttcct gctggacgag
480
gtctcggcgg gagatgcgcc gttcacgttc gtggacgaac aacgccgcga ccgcgcgcgc
540
gctgccgtcg ccaaggggt ctccgtcatc ctgaagtcgc aggtccggat cgacgggacg
600
ctgaccgcct ggtgcgcgca acacgacgag atcaccctgg caccgcgtcc ggcgcgcacc
660
ttcgagcacg cgtcgctcag cggcaacgag tctgtcgcga tcgtgcgctt cctgatgacc
720
cgtccgccga cgccagcgat cgtcgccgcg gtcgatgcgg cggtcgcctg gctcagacgc
780
gtccgcctcc ctgacggacg gtgggcccga ttctacgagt tcggtaccaa tcgtccgatc
840
ttctcggggc gagacagtgt cgtgcgctac aaactcgagg agatcgaaca ggaacgtcag
900
gagggctacg cgtggtacgg cacgtggccg aggacgcttg ttgagaagat gtaccctgca

960
tggaagtcgc ggcttccggg caagtag
987

<210> 46
<211> 328
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(20)

<221> DOMAIN
<222> (21)...(328)
<223> Catalytic domain

<400> 46
Met Thr Arg Arg Ala Phe Ile Ala Val Ile Cys Phe Phe Ala Ala Val
 1   5   10   15
Cys Ala His Ala Gln Ser Thr Val Arg Trp Lys Asp Val Leu Glu Gln
            20   25   30
Ser Glu Gly Trp Tyr Ser Thr Thr Ala Ala His Val Val Ala Asp Thr
        35   40   45
Val Leu Leu Tyr Gln Arg Pro Ser Gly Gly Trp Pro Lys Asp Ile Asp
    50   55   60
Met Thr Ala Pro Pro Ala Asp Arg Thr Pro Pro Ala Arg Pro Asp Ala
65   70   75   80
Thr Ile Asp Asn Gly Ala Thr Thr Thr Gln Ile Arg Leu Leu Ala Arg
                85   90   95
Ala Ala Ser Gly Ala Pro Ala Ala Ala Ala His Thr Tyr Thr Ala Ala
            100   105   110
Ala Leu Arg Gly Ile Asp Tyr Leu Leu Glu Ala Gln Tyr Pro Asn Gly
        115   120   125
Gly Trp Pro Gln Phe Phe Pro Leu Arg Lys Asp Tyr Ser Arg Tyr Val
    130   135   140
Thr Phe Asn Asp Asp Ala Met Met Asn Val Met Phe Leu Leu Asp Glu
145   150   155   160
Val Ser Ala Gly Asp Ala Pro Phe Thr Phe Val Asp Glu Gln Arg Arg
                165   170   175
Asp Arg Ala Arg Ala Ala Val Ala Lys Gly Val Ser Val Ile Leu Lys
            180   185   190
Ser Gln Val Arg Ile Asp Gly Thr Leu Thr Ala Trp Cys Ala Gln His
        195   200   205
Asp Glu Ile Thr Leu Ala Pro Arg Pro Ala Arg Thr Phe Glu His Ala
    210   215   220
Ser Leu Ser Gly Asn Glu Ser Val Ala Ile Val Arg Phe Leu Met Thr
225   230   235   240
Arg Pro Pro Thr Pro Ala Ile Val Ala Ala Val Asp Ala Ala Val Ala
                245   250   255
Trp Leu Arg Arg Val Arg Leu Pro Asp Gly Arg Trp Ala Arg Phe Tyr
            260   265   270
Glu Phe Gly Thr Asn Arg Pro Ile Phe Ser Gly Arg Asp Ser Val Val
        275   280   285
Arg Tyr Lys Leu Glu Glu Ile Glu Gln Glu Arg Gln Glu Gly Tyr Ala
    290   295   300
Trp Tyr Gly Thr Trp Pro Arg Thr Leu Val Glu Lys Met Tyr Pro Ala
305   310   315   320
Trp Lys Ser Arg Leu Pro Gly Lys

<210> 47
<211> 1077
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 47
atgaaaaatt ttaaaaatat tgtaggagcg ttacttatat ctgtaacgtt ttgtgtgcac
60
gggcaggtaa acaaaaaatc ctggcgggct attacacagt ctaacgacga tgcatggttt
120
gcatctgatg gagctgcaca gattgcagat aatgtattac tctatcagcg caatgttggc
180
ggatggccta aaaatattga aatgcaggaa ccgcttagtg aggccgacaa aaaaaagctg
240
atagatctta agtctacggc caaagaaagt actacagata atggggctac gtgtcaggaa
300
atggtattcc tctctaagat atataaacaa aagcccgaag agaagtataa agaggctttt
360
ttaaaaggac ttaattattt gcttgaagca cagtataaaa atggtggatg gccacagttc
420
tacccttaa aaaaaggtta ttatacccac attacctata atgacgattc tatggtaaac
480
attcttatga tcttaaagaa tattaaggaa gatgccaact attacagtat tacgccaagc
540
gataaagttt taaagcaggt atcgacagct tttgacagag gcattgactg cattctaaaa
600
acacagtaca agcaaaaggg tgtgcttaca agctggtgtg cccagcacga tgaggttaca
660
ttagaacctg caaatgcaag ggcttttgag ttggcatcac taagtggtaa agaatctgct
720
aaaataacgt tgttgctaat gtctgtaaaa aatccgtcta aagaggttgt tgctgctgta
780
gatgctgctg tggcgtggtt tgaaaaaaca aaaattgaag gcattaaagt agaagaagta
840
accggagctg atggcaaaaa ggatagggta gtagtacaaa gggctgatgc cgaaccattg
900
tgggcgcgtt ttatggaact ggataccaac aggccatttt tttgcgacag ggacggtata
960
aaaaaatatt cgcttgctga gataggtcat gaacgccgta acggatatgg ctggtacacc
1020
aacgaaccaa aagaagtttt aaagaaatac accaaatgga aaaacagtct taaatag
1077

<210> 48
<211> 358
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(21)

<221> DOMAIN
<222> (22)...(358)

<223> Catalytic domain

<400> 48
Met Lys Asn Phe Lys Asn Ile Val Gly Ala Leu Leu Ile Ser Val Thr
1 5 10 15
Phe Cys Val His Gly Gln Val Asn Lys Lys Ser Trp Arg Ala Ile Thr
20 25 30
Gln Ser Asn Asp Asp Ala Trp Phe Ala Ser Asp Gly Ala Ala Gln Ile
35 40 45
Ala Asp Asn Val Leu Leu Tyr Gln Arg Asn Val Gly Gly Trp Pro Lys
50 55 60
Asn Ile Glu Met Gln Glu Pro Leu Ser Glu Ala Asp Lys Lys Lys Leu
65 70 75 80
Ile Asp Leu Lys Ser Thr Ala Lys Glu Ser Thr Thr Asp Asn Gly Ala
85 90 95
Thr Cys Gln Glu Met Val Phe Leu Ser Lys Ile Tyr Lys Gln Lys Pro
100 105 110
Glu Glu Lys Tyr Lys Glu Ala Phe Leu Lys Gly Leu Asn Tyr Leu Leu
115 120 125
Glu Ala Gln Tyr Lys Asn Gly Gly Trp Pro Gln Phe Tyr Pro Leu Lys
130 135 140
Lys Gly Tyr Tyr Thr His Ile Thr Tyr Asn Asp Asp Ser Met Val Asn
145 150 155 160
Ile Leu Met Ile Leu Lys Asn Ile Lys Glu Asp Ala Asn Tyr Tyr Ser
165 170 175
Ile Thr Pro Ser Asp Lys Val Leu Lys Gln Val Ser Thr Ala Phe Asp
180 185 190
Arg Gly Ile Asp Cys Ile Leu Lys Thr Gln Tyr Lys Gln Lys Gly Val
195 200 205
Leu Thr Ser Trp Cys Ala Gln His Asp Glu Val Thr Leu Glu Pro Ala
210 215 220
Asn Ala Arg Ala Phe Glu Leu Ala Ser Leu Ser Gly Lys Glu Ser Ala
225 230 235 240
Lys Ile Thr Leu Leu Leu Met Ser Val Lys Asn Pro Ser Lys Glu Val
245 250 255
Val Ala Ala Val Asp Ala Ala Val Ala Trp Phe Glu Lys Thr Lys Ile
260 265 270
Glu Gly Ile Lys Val Glu Glu Val Thr Gly Ala Asp Gly Lys Lys Asp
275 280 285
Arg Val Val Val Gln Arg Ala Asp Ala Glu Pro Leu Trp Ala Arg Phe
290 295 300
Met Glu Leu Asp Thr Asn Arg Pro Phe Phe Cys Asp Arg Asp Gly Ile
305 310 315 320
Lys Lys Tyr Ser Leu Ala Glu Ile Gly His Glu Arg Arg Asn Gly Tyr
325 330 335
Gly Trp Tyr Thr Asn Glu Pro Lys Glu Val Leu Lys Lys Tyr Thr Lys
340 345 350
Trp Lys Asn Ser Leu Lys
355

<210> 49
<211> 1023
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 49
atgttaagtt tcatcgcggt atcagtgttt cataattact gcacagggca gacagcgtcc
60

accaaaaatt cagtggccga aaagatgctt cagtaccagt tgtcaaatgg cgcctggccc
120
aaacagttgg tagacaaaag tgtcgttgat tacagtcttc cattaacgaa agagcgccta
180
cagcagatca agaaaacaga tattgatcat gctacgctcg acaacagtgc gacaacccgg
240
gaaataactg aattgatcaa ggcttttaag gacactaaaa ataaggcata tttgactgct
300
gtagaaaagg ggattgcata tattttatcg gctcaatatg agaatggcgg atttccacaa
360
tactacccaa ataaattata ctatagagct gagataacat acaacgatga tgcgatgatc
420
aatgcattac tagtgcttta caaagtagcc aataagcgag aggggtttga ggctatcaat
480
cccatatttg tgtcaaaagc gcaaaaagca gttgaaaagg gtataacctg tatcctaaaa
540
acacaggtca tacaagacgg aaaaaggagt atttgggctg cgcaatacga tcagaacact
600
ttacaacctg ctcaggcaag aaagtttgaa ccagcttcat tgagcacaag tgaatctgtt
660
tccatcgttc gctttctcat gctacagcct gcaaccactg aaattaagca agcgatcgaa
720
catgcaatac aatggttcga acagcatgat attgaaggtt accgtttcga ccgcatacaa
780
gatagggtga ctggaaaata tcaacggcaa cttgtcgcag atcggacttc cacgatttgg
840
gcgcgatttt ataatctcga agacaaccgc ccattgtttg gagatcggga caatacaatc
900
aaatacaact ttgaggaggt ttcagaggag cgtagaaatg gctatgcttg gttcggcaac
960
tggccggaaa agctgatcca aaaggactat ccaaaatgga aaaaacaata caaaattaaa
1020
taa
1023

<210> 50
<211> 340
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(16)

<221> DOMAIN
<222> (17)...(340)
<223> Catalytic domain

<400> 50
Met Leu Ser Phe Ile Ala Val Ser Val Phe His Asn Tyr Cys Thr Gly
 1   5   10   15
Gln Thr Ala Ser Thr Lys Asn Ser Val Ala Glu Lys Met Leu Gln Tyr
            20   25   30
Gln Leu Ser Asn Gly Ala Trp Pro Lys Gln Leu Val Asp Lys Ser Val
        35   40   45
Val Asp Tyr Ser Leu Pro Leu Thr Lys Glu Arg Leu Gln Gln Ile Lys
    50   55   60
Lys Thr Asp Ile Asp His Ala Thr Leu Asp Asn Ser Ala Thr Thr Arg
65   70   75   80

Glu Ile Thr Glu Leu Ile Lys Ala Phe Lys Asp Thr Lys Asn Lys Ala
85 90 95
Tyr Leu Thr Ala Val Glu Lys Gly Ile Ala Tyr Ile Leu Ser Ala Gln
100 105 110
Tyr Glu Asn Gly Gly Phe Pro Gln Tyr Tyr Pro Asn Lys Leu Tyr Tyr
115 120 125
Arg Ala Glu Ile Thr Tyr Asn Asp Asp Ala Met Ile Asn Ala Leu Leu
130 135 140
Val Leu Tyr Lys Val Ala Asn Lys Arg Glu Gly Phe Glu Ala Ile Asn
145 150 155 160
Pro Ile Phe Val Ser Lys Ala Gln Lys Ala Val Glu Lys Gly Ile Thr
165 170 175
Cys Ile Leu Lys Thr Gln Val Ile Gln Asp Gly Lys Arg Ser Ile Trp
180 185 190
Ala Ala Gln Tyr Asp Gln Asn Thr Leu Gln Pro Ala Gln Ala Arg Lys
195 200 205
Phe Glu Pro Ala Ser Leu Ser Thr Ser Glu Ser Val Ser Ile Val Arg
210 215 220
Phe Leu Met Leu Gln Pro Ala Thr Thr Glu Ile Lys Gln Ala Ile Glu
225 230 235 240
His Ala Ile Gln Trp Phe Glu Gln His Asp Ile Glu Gly Tyr Arg Phe
245 250 255
Asp Arg Ile Gln Asp Arg Val Thr Gly Lys Tyr Gln Arg Gln Leu Val
260 265 270
Ala Asp Arg Thr Ser Thr Ile Trp Ala Arg Phe Tyr Asn Leu Glu Asp
275 280 285
Asn Arg Pro Leu Phe Gly Asp Arg Asp Asn Thr Ile Lys Tyr Asn Phe
290 295 300
Glu Glu Val Ser Glu Glu Arg Arg Asn Gly Tyr Ala Trp Phe Gly Asn
305 310 315 320
Trp Pro Glu Lys Leu Ile Gln Lys Asp Tyr Pro Lys Trp Lys Lys Gln
325 330 335
Tyr Lys Ile Lys
340

<210> 51
<211> 1131
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 51
gtgacgtggg atcagatcct tcgtcagcct gccgcctggt acggcggtcc ggaagcgcga
60
cggatcgcga atctggtcct gctgtaccag cgcgcgacgg ggggctggcc caagaacatc
120
gacatggcgc ggtcgttgtc tccggacgat cgcacgacgc tcgcggcgga acgggccctc
180
accgactcga cgatcgacaa tggatcgacg acgacgcagt tgcggtttct cgcgatggtg
240
cagcacgccc agcaggcacc cgtgcgcgac gccatcacgc acggcctgga ctatctgctg
300
aacgcgcaat actcgaacgg cggatggccg cagtactttc cgctccgaga cgactactcg
360
cgtcacatca cgttcaacga cgacgcgatg atcaatgtaa tgacggtgct acgcgatgtc
420
gcagaagctc gcatgcccct cgaagggatc gacgcggtcc gtcgggaccg ggcgcgtgtc
480
gccatcacgc gtggcatcga cgtgattctc gggacgcaaa tccgcgtcgg ggaccgtctg

540
acgggctggt gccagcagca tgacgagcgc tccctcgccc ccaccaaggc tcgcgcctac
600
gagcacccat cgatcgccag caaggaaacg gtaaccatca cgcgcttcct catgaccctc
660
gatcgcccga gtcagcagat catcgcggcg atcgaggcgg ctgtcgagtg gttgcgcgtg
720
gcgaccctgt cgggtgtgcg agttgagcgt cggccggacc cggcgagtcc gaccggatat
780
gacgtcgtcg ccgcgccgga tgccgccgca cctccgacct gggcacggtt ctacgagatc
840
ggcacgaacc gcccaatgtt ttccggccgc gacggcgtga tcagattccg gctcgcggac
900
atcgagattg agcgccgcac cggctacagc tggatgggcg actatgccgc gaggttgctg
960
aacgaggagt atccggcgtg ggcgaggcta cgccgggcga gctttcagaa cgccgagctg
1020
cacaaggagt ccggtgaagt cgtacacacg gcgatcgtgc acgatcttgc cttccttgat
1080
gtcgaagaca aagaccagcc gcagccgaaa gtgcttttcg ctgggcggta g
1131

<210> 52
<211> 376
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(376)
<223> Catalytic domain

<400> 52
Met Thr Trp Asp Gln Ile Leu Arg Gln Pro Ala Ala Trp Tyr Gly Gly
 1   5   10   15
Pro Glu Ala Arg Arg Ile Ala Asn Leu Val Leu Leu Tyr Gln Arg Ala
            20   25   30
Thr Gly Gly Trp Pro Lys Asn Ile Asp Met Ala Arg Ser Leu Ser Pro
        35   40   45
Asp Asp Arg Thr Thr Leu Ala Ala Glu Arg Ala Leu Thr Asp Ser Thr
    50   55   60
Ile Asp Asn Gly Ser Thr Thr Thr Gln Leu Arg Phe Leu Ala Met Val
65   70   75   80
Gln His Ala Gln Gln Ala Pro Val Arg Asp Ala Ile Thr His Gly Leu
                85   90   95
Asp Tyr Leu Leu Asn Ala Gln Tyr Ser Asn Gly Gly Trp Pro Gln Tyr
            100   105   110
Phe Pro Leu Arg Asp Asp Tyr Ser Arg His Ile Thr Phe Asn Asp Asp
        115   120   125
Ala Met Ile Asn Val Met Thr Val Leu Arg Asp Val Ala Glu Ala Arg
    130   135   140
Met Pro Phe Glu Gly Ile Asp Ala Val Arg Arg Asp Arg Ala Arg Val
145   150   155   160
Ala Ile Thr Arg Gly Ile Asp Val Ile Leu Gly Thr Gln Ile Arg Val
                165   170   175
Gly Asp Arg Leu Thr Gly Trp Cys Gln Gln His Asp Glu Arg Ser Leu
            180   185   190
Ala Pro Thr Lys Ala Arg Ala Tyr Glu His Pro Ser Ile Ala Ser Lys
        195   200   205

Glu Thr Val Thr Ile Thr Arg Phe Leu Met Thr Leu Asp Arg Pro Ser
210 215 220
Gln Gln Ile Ile Ala Ala Ile Glu Ala Ala Val Glu Trp Leu Arg Val
225 230 235 240
Ala Thr Leu Ser Gly Val Arg Val Glu Arg Arg Pro Asp Pro Ala Ser
245 250 255
Pro Thr Gly Tyr Asp Val Val Ala Ala Pro Asp Ala Ala Ala Pro Pro
260 265 270
Thr Trp Ala Arg Phe Tyr Glu Ile Gly Thr Asn Arg Pro Met Phe Ser
275 280 285
Gly Arg Asp Gly Val Ile Arg Phe Arg Leu Ala Asp Ile Glu Ile Glu
290 295 300
Arg Arg Thr Gly Tyr Ser Trp Met Gly Asp Tyr Ala Ala Arg Leu Leu
305 310 315 320
Asn Glu Glu Tyr Pro Ala Trp Ala Arg Leu Arg Arg Ala Ser Phe Gln
325 330 335
Asn Ala Glu Leu His Lys Glu Ser Gly Glu Val Val His Thr Ala Ile
340 345 350
Val His Asp Leu Ala Phe Leu Asp Val Glu Asp Lys Asp Gln Pro Gln
355 360 365
Pro Lys Val Leu Phe Ala Gly Arg
370 375

<210> 53
<211> 1977
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 53
atgaataact caacaaaaaa aatgattcgg ccactcaagg catcttttgc cttgggcgct
60
ctcgcactgg caatcgcatc accctcatgg gcggcttgct cttacagcgt aaccaataat
120
tggggctctg gctttaccgg agaaattaaa gtaaccaacg atacaacatc gactgtaaat
180
aattggtctg tgtcttggca ggaatcaggc gtgaccgtca ctaacgcatg gaatgcaaca
240
ctgagcggat caaatcctta taccgcaaca tcactcgggt ggaacggaac tctcgctcca
300
aaagcttcag caagttttgg ttttcaagca aatggaacag cgggcgcacc gaaagtaaat
360
ggaaccttgt gtggtaccag cacatcatca acaggtacat cctcagttgc accttcatcc
420
gtagcgagta gcgttgctgt atcaagcagt aaatcatcaa gctctgttgc aaccatcagt
480
agctctaaat ccagcagcag tgtgccgaca gtttcatcat tcactattca ggaagagcaa
540
gccggtttct gccgtgtaga tggcattgca actgaaagta ctaacactgg ctatacaggt
600
aatggctaca ccaacaccac taatgcgcaa ggcgctgcaa ttgaatgggc aattaatgct
660
cccaacagca gccgctacac cctcaccttc cgttatgcca atgctggtac cgctaatcgc
720
aatggttcgt tattaattaa cgacggaagc aatggtaact acacagtgca attgccaagt
780
accggcgcat gggcaacctg gcaaaccgtc agtgttgaag tggatttggt gcaaggcaat
840
aatattttga aactcgcttc gcttactgct gatggccttg cgaatataga ttcattaaaa

900
attgaaggcg cacaagccaa agctggtgta tgcagcacta cggtaagtag cagctcttcg
960
tcaattaaat caagttccag ttcatcatcg tccagctcaa ctgcagcagt aaaaacatta
1020
acactggatg gtaaccctgc tgcaaactgg tttaataaat ccagaaccaa gtggaatgtc
1080
agcagagctg acatcgtact ttcgtatcag caatcaaatg gtggctggcc aaaaaatttg
1140
gactacaact cggtaggctc aggtaatggt ggtagcgaca gcggcactat tgataatggt
1200
gcaaccataa ccgaaatggt gtacctcgct gaagtgtata aaaatggcgg gaataccaaa
1260
taccgcgacg ccgtgcgcag agcagcgaat tttattgtga gttcacaata cagcactggt
1320
gctttaccgc agttttatcc gctgaaaggt ggttacgcag atcacgctac ctttaatgat
1380
aatggtatgg cttacgcgtt gactgttctg gatttcgcgg taaataaacg cgcgccattt
1440
gataacgata ttttctctga ctctgaccgc agcaaattta aaactgctgt taccaaaggc
1500
gtcgattaca tattaaaagc gcaatggaaa cagaatggaa aattaaccgt atggtgcgca
1560
caacacggtg ctaatgatta tcaaccgaaa aaagcgcgtg cttacgagtt agaatcattg
1620
agtggtagtg aatctgtcgg tgtactcgct ttcttaatga ctcaaccaca aaccacgcaa
1680
attgaagcag ctgtgcgtgc aggtgtggcc tggtttaata gcccaagcac ctacttgaat
1740
aattacactt acgattcttc caaagcttcg accaatccaa tcgtgccaaa atccggaagc
1800
aaaatgtggt atcgctttta tgacctgaat accaaccgcg gtttcttcag tgatcgtgac
1860
ggcagcaagt tctacgacat cacccaaatg tcagaagagc gtcgcactgg ttacagttgg
1920
ggtggtgact acggcagctc gattatcagc ttcgcacaaa aagtgggata tctctaa
1977

<210> 54
<211> 658
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(31)

<221> BINDING
<222> (32)...(124)
<223> Carbohydrate binding module

<221> BINDING
<222> (180)...(303)
<223> Carbohydrate binding module

<221> DOMAIN
<222> (304)...(658)
<223> Catalytic domain

<400> 54

```
Met Asn Asn Ser Thr Lys Lys Met Ile Arg Pro Leu Lys Ala Ser Phe
 1               5                  10                  15
Ala Leu Gly Ala Leu Ala Leu Ala Ile Ala Ser Pro Ser Trp Ala Ala
            20                  25                  30
Cys Ser Tyr Ser Val Thr Asn Asn Trp Gly Ser Gly Phe Thr Gly Glu
        35                  40                  45
Ile Lys Val Thr Asn Asp Thr Thr Ser Thr Val Asn Asn Trp Ser Val
    50                  55                  60
Ser Trp Gln Glu Ser Gly Val Thr Val Thr Asn Ala Trp Asn Ala Thr
65                  70                  75                  80
Leu Ser Gly Ser Asn Pro Tyr Thr Ala Thr Ser Leu Gly Trp Asn Gly
                85                  90                  95
Thr Leu Ala Pro Lys Ala Ser Ala Ser Phe Gly Phe Gln Ala Asn Gly
            100                 105                 110
Thr Ala Gly Ala Pro Lys Val Asn Gly Thr Leu Cys Gly Thr Ser Thr
        115                 120                 125
Ser Ser Thr Gly Thr Ser Ser Val Ala Pro Ser Ser Val Ala Ser Ser
    130                 135                 140
Val Ala Val Ser Ser Ser Lys Ser Ser Ser Ser Val Ala Thr Ile Ser
145                 150                 155                 160
Ser Ser Lys Ser Ser Ser Ser Val Pro Thr Val Ser Ser Phe Thr Ile
                165                 170                 175
Gln Glu Glu Gln Ala Gly Phe Cys Arg Val Asp Gly Ile Ala Thr Glu
            180                 185                 190
Ser Thr Asn Thr Gly Tyr Thr Gly Asn Gly Tyr Thr Asn Thr Thr Asn
        195                 200                 205
Ala Gln Gly Ala Ala Ile Glu Trp Ala Ile Asn Ala Pro Asn Ser Ser
    210                 215                 220
Arg Tyr Thr Leu Thr Phe Arg Tyr Ala Asn Ala Gly Thr Ala Asn Arg
225                 230                 235                 240
Asn Gly Ser Leu Leu Ile Asn Asp Gly Ser Asn Gly Asn Tyr Thr Val
                245                 250                 255
Gln Leu Pro Ser Thr Gly Ala Trp Ala Thr Trp Gln Thr Val Ser Val
            260                 265                 270
Glu Val Asp Leu Val Gln Gly Asn Asn Ile Leu Lys Leu Ala Ser Leu
        275                 280                 285
Thr Ala Asp Gly Leu Ala Asn Ile Asp Ser Leu Lys Ile Glu Gly Ala
    290                 295                 300
Gln Ala Lys Ala Gly Val Cys Ser Thr Thr Val Ser Ser Ser Ser Ser
305                 310                 315                 320
Ser Ile Lys Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Ala Ala
                325                 330                 335
Val Lys Thr Leu Thr Leu Asp Gly Asn Pro Ala Ala Asn Trp Phe Asn
            340                 345                 350
Lys Ser Arg Thr Lys Trp Asn Val Ser Arg Ala Asp Ile Val Leu Ser
        355                 360                 365
Tyr Gln Gln Ser Asn Gly Gly Trp Pro Lys Asn Leu Asp Tyr Asn Ser
    370                 375                 380
Val Gly Ser Gly Asn Gly Gly Ser Asp Ser Gly Thr Ile Asp Asn Gly
385                 390                 395                 400
Ala Thr Ile Thr Glu Met Val Tyr Leu Ala Glu Val Tyr Lys Asn Gly
                405                 410                 415
Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg Arg Ala Ala Asn Phe Ile
            420                 425                 430
Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu Pro Gln Phe Tyr Pro Leu
        435                 440                 445
Lys Gly Gly Tyr Ala Asp His Ala Thr Phe Asn Asp Asn Gly Met Ala
    450                 455                 460
Tyr Ala Leu Thr Val Leu Asp Phe Ala Val Asn Lys Arg Ala Pro Phe
465                 470                 475                 480
```

Asp Asn Asp Ile Phe Ser Asp Ser Asp Arg Ser Lys Phe Lys Thr Ala
485 490 495
Val Thr Lys Gly Val Asp Tyr Ile Leu Lys Ala Gln Trp Lys Gln Asn
500 505 510
Gly Lys Leu Thr Val Trp Cys Ala Gln His Gly Ala Asn Asp Tyr Gln
515 520 525
Pro Lys Lys Ala Arg Ala Tyr Glu Leu Glu Ser Leu Ser Gly Ser Glu
530 535 540
Ser Val Gly Val Leu Ala Phe Leu Met Thr Gln Pro Gln Thr Thr Gln
545 550 555 560
Ile Glu Ala Ala Val Arg Ala Gly Val Ala Trp Phe Asn Ser Pro Ser
565 570 575
Thr Tyr Leu Asn Asn Tyr Thr Tyr Asp Ser Ser Lys Ala Ser Thr Asn
580 585 590
Pro Ile Val Pro Lys Ser Gly Ser Lys Met Trp Tyr Arg Phe Tyr Asp
595 600 605
Leu Asn Thr Asn Arg Gly Phe Phe Ser Asp Arg Asp Gly Ser Lys Phe
610 615 620
Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg Arg Thr Gly Tyr Ser Trp
625 630 635 640
Gly Gly Asp Tyr Gly Ser Ser Ile Ile Ser Phe Ala Gln Lys Val Gly
645 650 655
Tyr Leu

<210> 55
<211> 1125
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 55
gtggtcctag gtaataacgg cggcagcttg agttgcgtcc aatatattgt gattgtgaaa
60
ggacccggtg gacctcgacc gccggtgaaa ccggccgtcc aggcgcccgt tagggttacc
120
tggagcgcat gcctagtcca gcggcccgaa tggtacggga gtgacgaagc gatccgcatc
180
gcggacaacg tcctcctcta ccagcgcaac accggcgggt ggccgaagga catagatatg
240
gccgagccca tcccggaaca caggaagtcc tttttcctca ccgagaagga gcggaccgat
300
gactcgacca tcgacaacgg tgccaccgtg acccagctca agtatctcgc ccgcgtctac
360
aaggcgacca ggctggaacg gttcaaggag ggcttcctca aaggtctcga ctacctcttg
420
gccgcccagt acccgaacgg cggctggccc cagtattatc ctaacttgag gggctactac
480
gccaacatca cttataacga caatgccatg gtgaacgtgc tcaccctcct ccagagcatc
540
gccaaaaagg ccccggagta cgacttcgtc gacccggcgc gccgggagaa ggccgcccgg
600
gccgtggcga aagggatcga ctgcatcctc aagacccaga tccgtgtcaa tggaaaactt
660
accgcctggt gcgcccagca tgaccccaag acgctggcgc ccgcgccggc ccgttcgtat
720
gagcttgagt ccatcagcgg tttcgagagc gtcgggatcg tccggttctt aatgagcctc
780
gagaatccga gcccgaaggt catcgaggcg gtagaggccg ccgtgaaatg gttcgaggag

840
gtcaagctta ccgggatcaa ggtggtcgag aaacccgacc cgtcccttcc gggcggttac
900
gaccgcgtgg tggtcgaaga ccccaacgcg ccgcccatct gggcccggtt ctacgagatc
960
ggcaccaacc gtcccttctt ctgcggccgc gatggtatca aaaaatacag cctggcggag
1020
atcgaacacg aacgccgggt cggttactcc tggtacacca atgccccggc ctacctcatc
1080
gagaaggagt atccgctctg gcgggccaaa caccctacca agtaa
1125

<210> 56
<211> 374
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(374)
<223> Catalytic domain

<400> 56
Met Val Leu Gly Asn Asn Gly Gly Ser Leu Ser Cys Val Gln Tyr Ile
 1   5   10   15
Val Ile Val Lys Gly Pro Gly Gly Pro Arg Pro Pro Val Lys Pro Ala
            20   25   30
Val Gln Ala Pro Val Arg Val Thr Trp Ser Ala Cys Leu Val Gln Arg
        35   40   45
Pro Glu Trp Tyr Gly Ser Asp Glu Ala Ile Arg Ile Ala Asp Asn Val
    50   55   60
Leu Leu Tyr Gln Arg Asn Thr Gly Gly Trp Pro Lys Asp Ile Asp Met
65   70   75   80
Ala Glu Pro Ile Pro Glu His Arg Lys Ser Phe Phe Leu Thr Glu Lys
                85   90   95
Glu Arg Thr Asp Asp Ser Thr Ile Asp Asn Gly Ala Thr Val Thr Gln
            100   105   110
Leu Lys Tyr Leu Ala Arg Val Tyr Lys Ala Thr Arg Leu Glu Arg Phe
        115   120   125
Lys Glu Gly Phe Leu Lys Gly Leu Asp Tyr Leu Leu Ala Ala Gln Tyr
    130   135   140
Pro Asn Gly Gly Trp Pro Gln Tyr Tyr Pro Asn Leu Arg Gly Tyr Tyr
145   150   155   160
Ala Asn Ile Thr Tyr Asn Asp Asn Ala Met Val Asn Val Leu Thr Leu
                165   170   175
Leu Gln Ser Ile Ala Lys Lys Ala Pro Glu Tyr Asp Phe Val Asp Pro
            180   185   190
Ala Arg Arg Glu Lys Ala Ala Arg Ala Val Ala Lys Gly Ile Asp Cys
        195   200   205
Ile Leu Lys Thr Gln Ile Arg Val Asn Gly Lys Leu Thr Ala Trp Cys
    210   215   220
Ala Gln His Asp Pro Lys Thr Leu Ala Pro Ala Pro Ala Arg Ser Tyr
225   230   235   240
Glu Leu Glu Ser Ile Ser Gly Phe Glu Ser Val Gly Ile Val Arg Phe
                245   250   255
Leu Met Ser Leu Glu Asn Pro Ser Pro Lys Val Ile Glu Ala Val Glu
            260   265   270
Ala Ala Val Lys Trp Phe Glu Glu Val Lys Leu Thr Gly Ile Lys Val
        275   280   285

Val Glu Lys Pro Asp Pro Ser Leu Pro Gly Gly Tyr Asp Arg Val Val
290 295 300
Val Glu Asp Pro Asn Ala Pro Pro Ile Trp Ala Arg Phe Tyr Glu Ile
305 310 315 320
Gly Thr Asn Arg Pro Phe Phe Cys Gly Arg Asp Gly Ile Lys Lys Tyr
325 330 335
Ser Leu Ala Glu Ile Glu His Glu Arg Arg Val Gly Tyr Ser Trp Tyr
340 345 350
Thr Asn Ala Pro Ala Tyr Leu Ile Glu Lys Glu Tyr Pro Leu Trp Arg
355 360 365
Ala Lys His Pro Thr Lys
370

<210> 57
<211> 1170
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 57
atggacaaac gcgtcaaatg gattcatcag ctttcaaaag aagaagcaaa gcagttcgag
60
cccgaaaatt tcctcaaagg caaagacggc tggaatccga aaaaggcgga tgaccgctgg
120
ctcgaaaaaa caaaacctga ctggcagctc gttacgtgga acgacgcgtt acgccaggcg
180
ccgctctggt atcaaaccga tgaagcggcg cgcattgccg accaggtgat tttgtaccag
240
aaagacaacg gcggctggga aaaaaatctc gatatgacgg cgatgctcac gcaagccgaa
300
cgcgaaaagc tcgccaaaga aaaatcgaac acgtcggaaa cgacgatcga caaccgcacg
360
acctacacgc aagtcgcttt tctcgccaaa gtcattacgg gcagcttgca gaaaacgact
420
ccgccgacca atttcccgaa acataaggaa gctttttca agggcttgga ttacctgctc
480
gcgtcgcagt acgaatcggg cggctttccg cagttttatc cgctcaaaaa aggttattac
540
acgcacatca cgttcaacga cgatgcgatg attggcgttt tgaaggtttt gcgcgaaatc
600
gccaaaaaga aggaagacta tctttttgtt gacgaagaac gccgcctgaa agcggaaaaa
660
tcggtcgaaa aagcgctgcc gctgattctg aaattgcagg ttgaagtcgg cggcaaaaaa
720
acggtttggg cggcgcagta tgacgaaaac acttttaaac ccgcagcggc gcgaaagttt
780
gaaccggttt ctttaacggc gggcgaatcg gtcggcatcg tccggttttt aatgtacgat
840
tcaaagcccg accaggcgac gattgacgcg attgaatctg ccattcagtg gtatcgcgcg
900
aacaaaatcg aaggcattcg atgggtgcgc gaaaacggcg aaaaccgcgt cgtcaaggac
960
aaaaacgcgc cgccgatttg ggcgcggttt tacgaaatcg aaacgatgaa gccgattttc
1020
atcgggcgcg acgccatcat tcgttacgac gtgtctgaaa tcgaagccga gcgccgcaac
1080
ggctacgcgt ggtacgtctc ggagccgaac gagctgcttg aaaaagatta cccgaaatgg
1140
ctggaaaaaa ttaaaaaatc agtaaagtaa

1170

<210> 58
<211> 389
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(389)
<223> Catalytic domain

<400> 58
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Met Asp Lys Arg Val Lys Trp Ile His Gln Leu Ser Lys Glu Glu Ala
 1               5                  10                  15
Lys Gln Phe Glu Pro Glu Asn Phe Leu Lys Gly Lys Asp Gly Trp Asn
            20                  25                  30
Pro Lys Lys Ala Asp Asp Arg Trp Leu Glu Lys Thr Lys Pro Asp Trp
        35                  40                  45
Gln Leu Val Thr Trp Asn Asp Ala Leu Arg Gln Ala Pro Leu Trp Tyr
    50                  55                  60
Gln Thr Asp Glu Ala Ala Arg Ile Ala Asp Gln Val Ile Leu Tyr Gln
65                  70                  75                  80
Lys Asp Asn Gly Gly Trp Glu Lys Asn Leu Asp Met Thr Ala Met Leu
                85                  90                  95
Thr Gln Ala Glu Arg Glu Lys Leu Ala Lys Glu Lys Ser Asn Thr Ser
            100                 105                 110
Glu Thr Thr Ile Asp Asn Arg Thr Thr Tyr Thr Gln Val Ala Phe Leu
        115                 120                 125
Ala Lys Val Ile Thr Gly Ser Leu Gln Lys Thr Thr Pro Pro Thr Asn
    130                 135                 140
Phe Pro Lys His Lys Glu Ala Phe Phe Lys Gly Leu Asp Tyr Leu Leu
145                 150                 155                 160
Ala Ser Gln Tyr Glu Ser Gly Gly Phe Pro Gln Phe Tyr Pro Leu Lys
                165                 170                 175
Lys Gly Tyr Tyr Thr His Ile Thr Phe Asn Asp Asp Ala Met Ile Gly
            180                 185                 190
Val Leu Lys Val Leu Arg Glu Ile Ala Lys Lys Lys Glu Asp Tyr Leu
        195                 200                 205
Phe Val Asp Glu Glu Arg Arg Leu Lys Ala Glu Lys Ser Val Glu Lys
    210                 215                 220
Ala Leu Pro Leu Ile Leu Lys Leu Gln Val Glu Val Gly Gly Lys Lys
225                 230                 235                 240
Thr Val Trp Ala Ala Gln Tyr Asp Glu Asn Thr Phe Lys Pro Ala Ala
                245                 250                 255
Ala Arg Lys Phe Glu Pro Val Ser Leu Thr Ala Gly Glu Ser Val Gly
            260                 265                 270
Ile Val Arg Phe Leu Met Tyr Asp Ser Lys Pro Asp Gln Ala Thr Ile
        275                 280                 285
Asp Ala Ile Glu Ser Ala Ile Gln Trp Tyr Arg Ala Asn Lys Ile Glu
    290                 295                 300
Gly Ile Arg Trp Val Arg Glu Asn Gly Glu Asn Arg Val Val Lys Asp
305                 310                 315                 320
Lys Asn Ala Pro Pro Ile Trp Ala Arg Phe Tyr Glu Ile Glu Thr Met
                325                 330                 335
Lys Pro Ile Phe Ile Gly Arg Asp Ala Ile Ile Arg Tyr Asp Val Ser
            340                 345                 350
Glu Ile Glu Ala Glu Arg Arg Asn Gly Tyr Ala Trp Tyr Val Ser Glu
        355                 360                 365
```

Pro Asn Glu Leu Leu Glu Lys Asp Tyr Pro Lys Trp Leu Glu Lys Ile
370 375 380
Lys Lys Ser Val Lys
385

<210> 59
<211> 1080
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 59
atgagaatcc ggtcctcttc aatcgcgttc ggcctgattt gcagtctggc gctaagggtg
60
cctgcgcaag cgcaggtcac cgtgcgctgg gcggacgtcc tgaaccagcc cgccgcctgg
120
tatggcaccg atgaagcccg tcgaattgcc gaccacgtgc tcgagcatca acgagcggaa
180
ggcggatggc caaagaacac ggacatgacc gcagcgcccg atccggcggt gctcacagcc
240
gcgcgagtga agccagactc gacgatcgat aacggcgcga ccgtcactga aatgcgcgtc
300
ctcgcgcgcg tctaccgttc atcacccgat ccccgttatc gcgatgcgct gctcaagggt
360
ctcgactatc tgttggcagc gcagtatgcc aacggcggct ggccgcagtt ctacccgctc
420
cggcaggact attcgcgcta tatcacgttc aacgacaacg cgatgatcaa tgtcgtgacg
480
ctgctctcag acgtcgctgc cggaaatggc gactgggcgt ttgctgatgc cagccggcgc
540
gagaaaagcc ggacggctgt agagaaggcc gtagaagtca tcctgcgcgc gcaggtgaga
600
gttgacggcc ggctgaccgc gtggtgcgcc caacacgacg aggtgacact cgagccgcgc
660
aaggcccgcg cctacgaaca tccgtcgctg agcggacagg agacggtggg gatcatccgg
720
tttctcatga cccgcgataa accggatcag agagtcgtcg atgcaatcga ggcgtcagtg
780
gcatggctga aggcggtgca gctcaaagga cttcgcgtcg accagcgccg cgatccctcg
840
ctgccggagg ggcgtgacgt ggtgaccgtc gctgacccgt cggcgccgcc gctctgggcg
900
cgcttctacg aaatcgggac caatcgcccg atcttctctg gacgcgacgg cgtgatccga
960
tactcgctgg cagagatcga gcacgaacgc cggatagggt acgcctggct cggaacctgg
1020
cccgcgaagc tgctcgatac cgaataccca tcctggcgac ggactcaaca aaggccgtga
1080

<210> 60
<211> 359
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(24)

<221> DOMAIN
<222> (25)...(359)
<223> Catalytic domain

<400> 60
Met Arg Ile Arg Ser Ser Ser Ile Ala Phe Gly Leu Ile Cys Ser Leu
 1   5   10   15
Ala Leu Arg Val Pro Ala Gln Ala Gln Val Thr Val Arg Trp Ala Asp
            20   25   30
Val Leu Asn Gln Pro Ala Ala Trp Tyr Gly Thr Asp Glu Ala Arg Arg
        35   40   45
Ile Ala Asp His Val Leu Glu His Gln Arg Ala Glu Gly Gly Trp Pro
    50   55   60
Lys Asn Thr Asp Met Thr Ala Ala Pro Asp Pro Ala Val Leu Thr Ala
65   70   75   80
Ala Arg Val Lys Pro Asp Ser Thr Ile Asp Asn Gly Ala Thr Val Thr
                85   90   95
Glu Met Arg Val Leu Ala Arg Val Tyr Arg Ser Ser Pro Asp Pro Arg
            100   105   110
Tyr Arg Asp Ala Leu Leu Lys Gly Leu Asp Tyr Leu Leu Ala Ala Gln
        115   120   125
Tyr Ala Asn Gly Gly Trp Pro Gln Phe Tyr Pro Leu Arg Gln Asp Tyr
    130   135   140
Ser Arg Tyr Ile Thr Phe Asn Asp Asn Ala Met Ile Asn Val Val Thr
145   150   155   160
Leu Leu Ser Asp Val Ala Ala Gly Asn Gly Asp Trp Ala Phe Ala Asp
                165   170   175
Ala Ser Arg Arg Glu Lys Ser Arg Thr Ala Val Glu Lys Ala Val Glu
            180   185   190
Val Ile Leu Arg Ala Gln Val Arg Val Asp Gly Arg Leu Thr Ala Trp
        195   200   205
Cys Ala Gln His Asp Glu Val Thr Leu Glu Pro Arg Lys Ala Arg Ala
    210   215   220
Tyr Glu His Pro Ser Leu Ser Gly Gln Glu Thr Val Gly Ile Ile Arg
225   230   235   240
Phe Leu Met Thr Arg Asp Lys Pro Asp Gln Arg Val Val Asp Ala Ile
                245   250   255
Glu Ala Ser Val Ala Trp Leu Lys Ala Val Gln Leu Lys Gly Leu Arg
            260   265   270
Val Asp Gln Arg Arg Asp Pro Ser Leu Pro Glu Gly Arg Asp Val Val
        275   280   285
Thr Val Ala Asp Pro Ser Ala Pro Pro Leu Trp Ala Arg Phe Tyr Glu
    290   295   300
Ile Gly Thr Asn Arg Pro Ile Phe Ser Gly Arg Asp Gly Val Ile Arg
305   310   315   320
Tyr Ser Leu Ala Glu Ile Glu His Glu Arg Arg Ile Gly Tyr Ala Trp
                325   330   335
Leu Gly Thr Trp Pro Ala Lys Leu Leu Asp Thr Glu Tyr Pro Ser Trp
            340   345   350
Arg Arg Thr Gln Gln Arg Pro
        355

<210> 61
<211> 1224
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 61
gtggaattac cagtaaccgg cgcatgggca acctggcaaa ccgcaactgt tgaaattgat
60
ttggtgcaag gtaacaacct gttaaaactt tctgcgatca cggctgatgg tttggcaaat
120
atcgattcgt tgaaaattga cggcgcacaa accaaagccg gcgtgtgcag cactgtggca
180
agcagcagct cttcatccgt tgcttcatcg attaaatcaa gctccagttc atcctcttcc
240
agttcaacga cgacggtaaa aacattaaca ctggatggca accccgcagc aaactggttt
300
aacaaatcca gaaccaaatg gaataccagc agagccgatg ttgtactttc ctatcaacaa
360
tccaacggcg gctggccaaa aaatctcgat tacaattcag taagcgcagg taatggcggc
420
agcgatagcg gcaccatcga taacggtgca accattactg aaatggttta tctcgcggaa
480
gtttacaaaa atggcaacaa caccaagtat cgcgatgcgg tgcgcagagc cgcaaatttt
540
attgtcagct cgcaatacag cactggtgca ttaccacaat tttatccatt gaaaggcggc
600
tatgcagacc acgccacctt taacgataac ggcatggcat atgcattaac ggtattggat
660
tttgcagtca acaaacgcgc cccatttgat actgatgttt tctccgattc tgatcgcgcg
720
aaattcaaaa ccgctgttgc caaaggtgtg gattacattt tgaaagcgca gtggaaacaa
780
aacggaaaat taaccgtgtg gtgtgcacaa catggtgcta ccgattatca accgaaaaaa
840
gcgcgcgcct atgaattgga atcactgagt ggcagcgaat ctgttggtgt actcgctttc
900
ttgatgaccc aaccgcaaac cgcacaaatt gaagccgctg taaaagccgg tgtagcctgg
960
ttcaatagcc ccaacacgta tttgaacaat tacacttacg actcttcaaa agcgtcaact
1020
aatccaatag ttgccaagtc tggaagcaaa atgtggtatc gcttttacga tttaaatacc
1080
aatcgtggct tcttcagtga tcgcgatggc agcaaattct atgacatcac ccagatgtca
1140
gaagagcgtc gcactggata tagctggggt ggtgattacg gcacgtcgat tatttccttc
1200
gcgcaaaaag tgggatatct gtaa
1224

<210> 62
<211> 407
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (0)...(407)
<223> Catalytic domain

<400> 62
Met Glu Leu Pro Val Thr Gly Ala Trp Ala Thr Trp Gln Thr Ala Thr
 1   5   10   15
Val Glu Ile Asp Leu Val Gln Gly Asn Asn Leu Leu Lys Leu Ser Ala
            20   25   30

Ile Thr Ala Asp Gly Leu Ala Asn Ile Asp Ser Leu Lys Ile Asp Gly
35 40 45
Ala Gln Thr Lys Ala Gly Val Cys Ser Thr Val Ala Ser Ser Ser Ser
50 55 60
Ser Ser Val Ala Ser Ser Ile Lys Ser Ser Ser Ser Ser Ser Ser Ser
65 70 75 80
Ser Ser Thr Thr Thr Val Lys Thr Leu Thr Leu Asp Gly Asn Pro Ala
85 90 95
Ala Asn Trp Phe Asn Lys Ser Arg Thr Lys Trp Asn Thr Ser Arg Ala
100 105 110
Asp Val Val Leu Ser Tyr Gln Gln Ser Asn Gly Gly Trp Pro Lys Asn
115 120 125
Leu Asp Tyr Asn Ser Val Ser Ala Gly Asn Gly Gly Ser Asp Ser Gly
130 135 140
Thr Ile Asp Asn Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala Glu
145 150 155 160
Val Tyr Lys Asn Gly Asn Asn Thr Lys Tyr Arg Asp Ala Val Arg Arg
165 170 175
Ala Ala Asn Phe Ile Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu Pro
180 185 190
Gln Phe Tyr Pro Leu Lys Gly Gly Tyr Ala Asp His Ala Thr Phe Asn
195 200 205
Asp Asn Gly Met Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala Val Asn
210 215 220
Lys Arg Ala Pro Phe Asp Thr Asp Val Phe Ser Asp Ser Asp Arg Ala
225 230 235 240
Lys Phe Lys Thr Ala Val Ala Lys Gly Val Asp Tyr Ile Leu Lys Ala
245 250 255
Gln Trp Lys Gln Asn Gly Lys Leu Thr Val Trp Cys Ala Gln His Gly
260 265 270
Ala Thr Asp Tyr Gln Pro Lys Lys Ala Arg Ala Tyr Glu Leu Glu Ser
275 280 285
Leu Ser Gly Ser Glu Ser Val Gly Val Leu Ala Phe Leu Met Thr Gln
290 295 300
Pro Gln Thr Ala Gln Ile Glu Ala Ala Val Lys Ala Gly Val Ala Trp
305 310 315 320
Phe Asn Ser Pro Asn Thr Tyr Leu Asn Asn Tyr Thr Tyr Asp Ser Ser
325 330 335
Lys Ala Ser Thr Asn Pro Ile Val Ala Lys Ser Gly Ser Lys Met Trp
340 345 350
Tyr Arg Phe Tyr Asp Leu Asn Thr Asn Arg Gly Phe Phe Ser Asp Arg
355 360 365
Asp Gly Ser Lys Phe Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg Arg
370 375 380
Thr Gly Tyr Ser Trp Gly Gly Asp Tyr Gly Thr Ser Ile Ile Ser Phe
385 390 395 400
Ala Gln Lys Val Gly Tyr Leu
405

<210> 63
<211> 1023
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 63
atgttaagtt tcatcgcggt atcagtgttt cataattact gtacagggca gactgcgtcc
60
accaaaaatt cagtggccga aaagatgctt cagtaccagt tgtcaaatgg cgcctggccc

120
aaacagttgg tagacaaaag tgtcgttgat tacagtcttc cattaacgaa agagctccta
180
cagcagatca agaaaacaga tattgatcat gctacgctcg acaacagtgc gacaacccgg
240
gaaataactg aattgatcaa ggcttttaag gacactaaaa ataaggcata tttgactgct
300
gcagaaaagg ggattgcata tattttatcg gctcaatatg agaatggcgg atttccacaa
360
tactacccaa ataaattata ctatagagct gagataacat acaacgatga tgcgatgatc
420
aatgcattac tagtgcttta caaagtagcc aataagcgag aggggtttga ggctatcaat
480
cccatatttg tgtcaaaagc gcaaaaagca gttgaaaagg gtataacctg tatcctaaaa
540
acacaggtca tacaagacgg aaaaaggagt atttgggctg cgcaatacga tcagaacact
600
ttacaacctg ctcaggcaag aaagtttgaa ccagcttcat tgagcacaag tgaatctgtt
660
tccatcgttc gctttctcat gctacagcct gcaaccactg aaattaagca agcgatcgaa
720
catgcaatac aatggttcga acagcatgat attgaaggtt accgtttcga ccgcatacaa
780
gatagggtga ctggaaaata tcaacggcag cttgtcgctg atcggacttc cacgatttgg
840
gcgcgatttt ataatctcga agacaaccgt ccattgtttg gagatcggga caatacaatc
900
aaatacaact ttgaggaggt ttcagaggag cgtagaaatg gctatgcttg gttcggcaac
960
tggccggaaa agctgatcca aaaggactat ccaaaatgga aaaaacaata caaaattcaa
1020
taa
1023

<210> 64
<211> 340
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(16)

<221> DOMAIN
<222> (17)...(340)
<223> Catalytic domain

<400> 64
Met Leu Ser Phe Ile Ala Val Ser Val Phe His Asn Tyr Cys Thr Gly
 1   5   10   15
Gln Thr Ala Ser Thr Lys Asn Ser Val Ala Glu Lys Met Leu Gln Tyr
            20   25   30
Gln Leu Ser Asn Gly Ala Trp Pro Lys Gln Leu Val Asp Lys Ser Val
        35   40   45
Val Asp Tyr Ser Leu Pro Leu Thr Lys Glu Leu Leu Gln Gln Ile Lys
    50   55   60
Lys Thr Asp Ile Asp His Ala Thr Leu Asp Asn Ser Ala Thr Thr Arg
65   70   75   80
Glu Ile Thr Glu Leu Ile Lys Ala Phe Lys Asp Thr Lys Asn Lys Ala

```
                85                  90                  95
Tyr Leu Thr Ala Ala Glu Lys Gly Ile Ala Tyr Ile Leu Ser Ala Gln
            100                 105                 110
Tyr Glu Asn Gly Gly Phe Pro Gln Tyr Tyr Pro Asn Lys Leu Tyr Tyr
        115                 120                 125
Arg Ala Glu Ile Thr Tyr Asn Asp Asp Ala Met Ile Asn Ala Leu Leu
    130                 135                 140
Val Leu Tyr Lys Val Ala Asn Lys Arg Glu Gly Phe Glu Ala Ile Asn
145                 150                 155                 160
Pro Ile Phe Val Ser Lys Ala Gln Lys Ala Val Glu Lys Gly Ile Thr
                165                 170                 175
Cys Ile Leu Lys Thr Gln Val Ile Gln Asp Gly Lys Arg Ser Ile Trp
            180                 185                 190
Ala Ala Gln Tyr Asp Gln Asn Thr Leu Gln Pro Ala Gln Ala Arg Lys
        195                 200                 205
Phe Glu Pro Ala Ser Leu Ser Thr Ser Glu Ser Val Ser Ile Val Arg
    210                 215                 220
Phe Leu Met Leu Gln Pro Ala Thr Thr Glu Ile Lys Gln Ala Ile Glu
225                 230                 235                 240
His Ala Ile Gln Trp Phe Glu Gln His Asp Ile Glu Gly Tyr Arg Phe
                245                 250                 255
Asp Arg Ile Gln Asp Arg Val Thr Gly Lys Tyr Gln Arg Gln Leu Val
            260                 265                 270
Ala Asp Arg Thr Ser Thr Ile Trp Ala Arg Phe Tyr Asn Leu Glu Asp
        275                 280                 285
Asn Arg Pro Leu Phe Gly Asp Arg Asp Asn Thr Ile Lys Tyr Asn Phe
    290                 295                 300
Glu Glu Val Ser Glu Glu Arg Arg Asn Gly Tyr Ala Trp Phe Gly Asn
305                 310                 315                 320
Trp Pro Glu Lys Leu Ile Gln Lys Asp Tyr Pro Lys Trp Lys Lys Gln
                325                 330                 335
Tyr Lys Ile Gln
            340
```

<210> 65
<211> 1311
<212> DNA
<213> Bacteria

<400> 65

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gtgaaccgac gtacccgcct gggagcggtc gccgcgaccg ccctcgccct gacggtcacc
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gccccccgccg ccggtgccca cgccgccgct ccccacgccg cgccacgccc ggtcgccgat
120
ccggctcgcg ccacgctgcc cgccggcgac ggctgggcgt ccgaggggac cggcacgacc
180
ggtggggccg ccgccgaggc ctcccgggtc ttcaccgtcg ccacctggga ggagttccgg
240
gccgcgctcg cggtgcccgg ctccgagccc aggatcgtca aggtggtggg cacgctgaac
300
gccaccgccg ccggctgcgg cgccttcgag gcgccgggct acgacttcgc ccgctacctc
360
gccgactacg acccggccgt gtgggggtac gagaaggagg tcagcggccc gcaggaggag
420
ctgcgggcgg cgtccgcgac cgcgcagggc caggccatca aggtcaaggt gccggcgaac
480
accacgatcg tcggggtcgg caggcacgcg gggatcacgg gcggcagcct ccaggtgcag
540
ggcgtcgaca acgtcgtggt ccgcaacctg acgctggaga gcccgctcga ctgcttcccg
600
cagtgggacc cgaccgacgg cgcgaccggg gcgtggaact ccgagtacga cagcctcgtc
```

660
gtgtacggct ccacccatgt ctggatcgac cacaacacct tcaccgacgg cgcccacccg
720
gacagttcgc tgccctcgta ctacggcgag gtctaccagc agcacgacgg cgaactggac
780
gtcgtgcggg gcgcggacct cgtcacggtc tcgtggaacg ccttcaccga ccacgacaag
840
accctgatga tcggcaacag cgacagcgcg ggcgccaccg accggggcaa gctgcgggtc
900
accctgcacc acaacctgtt cgagaacgtc gtcgagcggg cgccccgggt caggttcggg
960
caggtcgacg cgtacaacaa ccacttcgtc gtgccgagtt cggcctacgc gtacagcctg
1020
ggcgtcgggc aggagtccca gctcttcgcg gagaagaacg cgttcaccct cgccgggggc
1080
gtgccggccg ggaagatcct caagaagtgg aaggacgcgc ccgtcaccac cgtcggcaac
1140
tacgtgaacg gcaggccggt cgacctgctc gccgtccaca acacccagtt cccggaggag
1200
cagttgcggg ccgacgcggg ctggaccccc gtcctgcgca ccagggtcga ccacccgagg
1260
gccgtccccg cgctcgtcga ccaccgcgcg ggcgccggcc gctcctgctg a
1311

<210> 66
<211> 436
<212> PRT
<213> Bacteria

<220>

<221> SIGNAL
<222> (1)...(28)

<221> DOMAIN
<222> (29)...(436)
<223> Catalytic domain

<400> 66
Met Asn Arg Arg Thr Arg Leu Gly Ala Val Ala Ala Thr Ala Leu Ala
 1   5   10   15
Leu Thr Val Thr Ala Pro Ala Ala Gly Ala His Ala Ala Ala Pro His
            20   25   30
Ala Ala Pro Arg Pro Val Ala Asp Pro Ala Arg Ala Thr Leu Pro Ala
        35   40   45
Gly Asp Gly Trp Ala Ser Glu Gly Thr Gly Thr Thr Gly Gly Ala Ala
    50   55   60
Ala Glu Ala Ser Arg Val Phe Thr Val Ala Thr Trp Glu Glu Phe Arg
65   70   75   80
Ala Ala Leu Ala Val Pro Gly Ser Glu Pro Arg Ile Val Lys Val Val
                85   90   95
Gly Thr Leu Asn Ala Thr Ala Ala Gly Cys Gly Ala Phe Glu Ala Pro
            100   105   110
Gly Tyr Asp Phe Ala Arg Tyr Leu Ala Asp Tyr Asp Pro Ala Val Trp
        115   120   125
Gly Tyr Glu Lys Glu Val Ser Gly Pro Gln Glu Glu Leu Arg Ala Ala
    130   135   140
Ser Ala Thr Ala Gln Gly Gln Ala Ile Lys Val Lys Val Pro Ala Asn
145   150   155   160
Thr Thr Ile Val Gly Val Gly Arg His Ala Gly Ile Thr Gly Gly Ser
                165   170   175

```
Leu Gln Val Gln Gly Val Asp Asn Val Val Val Arg Asn Leu Thr Leu
            180                 185                 190
Glu Ser Pro Leu Asp Cys Phe Pro Gln Trp Asp Pro Thr Asp Gly Ala
        195                 200                 205
Thr Gly Ala Trp Asn Ser Glu Tyr Asp Ser Leu Val Val Tyr Gly Ser
    210                 215                 220
Thr His Val Trp Ile Asp His Asn Thr Phe Thr Asp Gly Ala His Pro
225                 230                 235                 240
Asp Ser Ser Leu Pro Ser Tyr Tyr Gly Glu Val Tyr Gln Gln His Asp
                245                 250                 255
Gly Glu Leu Asp Val Val Arg Gly Ala Asp Leu Val Thr Val Ser Trp
            260                 265                 270
Asn Ala Phe Thr Asp His Asp Lys Thr Leu Met Ile Gly Asn Ser Asp
        275                 280                 285
Ser Ala Gly Ala Thr Asp Arg Gly Lys Leu Arg Val Thr Leu His His
    290                 295                 300
Asn Leu Phe Glu Asn Val Val Glu Arg Ala Pro Arg Val Arg Phe Gly
305                 310                 315                 320
Gln Val Asp Ala Tyr Asn Asn His Phe Val Val Pro Ser Ser Ala Tyr
                325                 330                 335
Ala Tyr Ser Leu Gly Val Gly Gln Glu Ser Gln Leu Phe Ala Glu Lys
            340                 345                 350
Asn Ala Phe Thr Leu Ala Gly Gly Val Pro Ala Gly Lys Ile Leu Lys
        355                 360                 365
Lys Trp Lys Asp Ala Pro Val Thr Thr Val Gly Asn Tyr Val Asn Gly
    370                 375                 380
Arg Pro Val Asp Leu Leu Ala Val His Asn Thr Gln Phe Pro Glu Glu
385                 390                 395                 400
Gln Leu Arg Ala Asp Ala Gly Trp Thr Pro Val Leu Arg Thr Arg Val
                405                 410                 415
Asp His Pro Arg Ala Val Pro Ala Leu Val Asp His Arg Ala Gly Ala
            420                 425                 430
Gly Arg Ser Cys
        435
```

<210> 67
<211> 1995
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 67
atgaaaaatt caaaaactgt ttttactgca caaaaaaaac tcatgcactc ttgcattgcc
60
gccgctatcg gcttggcgat aagttcaggt gcttggtcag cttgtactta cactgtcacc
120
aataattggg gttctggctt caccggtgaa atcaaagtta ccaacaacac atcatcggct
180
gtaaatggtt ggtctgtgtc ttggcaggaa tcaggcgcat cagtcaccaa ctcatggaac
240
gcaactctga gcggatcaaa tccttatacg gcagccgcct taggttggaa tgcaactctc
300
gcacccggtg cttctgccag ttttggcttt caagcaaatg gcactgctag cgcacctaaa
360
gtgaatggca ctttatgtgg aacagctact tcatcaacac ctgcgtcatc cagcagtgtt
420
gcgagttcgg ttaaatcaag cgcacccgtt tcgtccagca gtaaatcatc cagctcaatc
480
actgtgagta gtagttctat cgccagcagc agcgcaccaa gtgtttcttc attaacaatt

540
caggaagagc aagctggctt ctgtcgtgtt gatggcattg caacagaaag caccaacacc
600
ggctttaccg gcaacggcta taccaatgca aacaacgcac aaggtgcagc gattgaatgg
660
gcggtaaatg caccgagcag tggccgctac acactcacat tccgttttgc aaatggcggc
720
actgcagcac gcaatggttc actgttaatt aacggcggta gcaatggtaa ctacaccgtg
780
gatttaccac taaccggcgc atgggcgact tggcaaacag cgactgtaga aatcgatttg
840
gtacaaggca ccaacacgct gaaactttct gcattaaccg cagatggctt agctaatatc
900
gattcattaa aaattgatgg caaccaaccg aaagcaggca cttgcagcaa tacatcaagc
960
agtgttgcca gcagttcttc atccgttaaa tccagttcaa gttcttcatc aagctcatcc
1020
accactgcaa aaatgctgac tcttgatggc aaccccgccg caagttggtt caacaaatcc
1080
agaaccaaat ggaatagcag tcgtgcggac attgtgttgt cttaccagca agctaacggc
1140
ggctggccaa aaaatctgga ttacaactca gtaagcgcag gtaatggtgg tagcgacagc
1200
ggcactatcg acaacggcgc aaccatcacg gaaatggttt atctcgcaga agtttataaa
1260
aacgggggca atacaaaata tcgcgatgca gtacgtaaag cggcaaactt tattgtgagt
1320
tcgcaataca gcactggtgc gttaccacaa ttttacccat tgaaaggtgg ttatgcagat
1380
cacgccacct ttaacgataa cggcatggct tacgcattaa cggtattgga ttttgcggtg
1440
aacaaacgtg cgccgtttga taacgatgta ttttctgatg cagaccgcgc aaaattcaaa
1500
actgccgtga ccaaaggtat tgattacatt ttgaaagccc aatggaaaca aaatggaaaa
1560
ctcaccgcat ggtgtgcgca acacggagca aacgactatc aaccaaaagc ggcgcgtgct
1620
tatgagttag tatctttaag cggcagcgaa tccgttggca tcatcgcttt cctgatgacc
1680
caaccacaaa ctgcgcaaat cgaagcagcg gttaaagccg gtgtaaactg gttcgctagc
1740
ccgaatacat acttggctaa ttacacctac gactcgtcaa aagcctctac caatccgatt
1800
gtgtacaaat ccggcagcag aatgtggtat cgcttctacg atctgaacac caatcgcgga
1860
ttctttagtg atcgcgatgg cagcaaattc tatgacatca ctcaaatgtc tgaagaacgt
1920
cgcaccggct acagctgggg cggttcttac ggtgaatcga ttatcagctt cgcgcaaaaa
1980
gtgggttatc tctaa
1995

<210> 68
<211> 664
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(32)

<221> BINDING
<222> (33)...(126)
<223> Carbohydrate binding module

<221> BINDING
<222> (184)...(307)
<223> Carbohydrate binding module

<221> DOMAIN
<222> (308)...(664)
<223> Catalytic domain

<400> 68

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Met Lys Asn Ser Lys Thr Val Phe Thr Ala Gln Lys Lys Leu Met His
 1               5                  10                  15
Ser Cys Ile Ala Ala Ala Ile Gly Leu Ala Ile Ser Ser Gly Ala Trp
            20                  25                  30
Ser Ala Cys Thr Tyr Thr Val Thr Asn Asn Trp Gly Ser Gly Phe Thr
        35                  40                  45
Gly Glu Ile Lys Val Thr Asn Asn Thr Ser Ser Ala Val Asn Gly Trp
    50                  55                  60
Ser Val Ser Trp Gln Glu Ser Gly Ala Ser Val Thr Asn Ser Trp Asn
65                  70                  75                  80
Ala Thr Leu Ser Gly Ser Asn Pro Tyr Thr Ala Ala Ala Leu Gly Trp
                85                  90                  95
Asn Ala Thr Leu Ala Pro Gly Ala Ser Ala Ser Phe Gly Phe Gln Ala
            100                 105                 110
Asn Gly Thr Ala Ser Ala Pro Lys Val Asn Gly Thr Leu Cys Gly Thr
        115                 120                 125
Ala Thr Ser Ser Thr Pro Ala Ser Ser Ser Ser Val Ala Ser Ser Val
    130                 135                 140
Lys Ser Ser Ala Pro Val Ser Ser Ser Ser Lys Ser Ser Ser Ser Ile
145                 150                 155                 160
Thr Val Ser Ser Ser Ser Ile Ala Ser Ser Ser Ala Pro Ser Val Ser
                165                 170                 175
Ser Leu Thr Ile Gln Glu Glu Gln Ala Gly Phe Cys Arg Val Asp Gly
            180                 185                 190
Ile Ala Thr Glu Ser Thr Asn Thr Gly Phe Thr Gly Asn Gly Tyr Thr
        195                 200                 205
Asn Ala Asn Asn Ala Gln Gly Ala Ala Ile Glu Trp Ala Val Asn Ala
    210                 215                 220
Pro Ser Ser Gly Arg Tyr Thr Leu Thr Phe Arg Phe Ala Asn Gly Gly
225                 230                 235                 240
Thr Ala Ala Arg Asn Gly Ser Leu Leu Ile Asn Gly Gly Ser Asn Gly
                245                 250                 255
Asn Tyr Thr Val Asp Leu Pro Leu Thr Gly Ala Trp Ala Thr Trp Gln
            260                 265                 270
Thr Ala Thr Val Glu Ile Asp Leu Val Gln Gly Thr Asn Thr Leu Lys
        275                 280                 285
Leu Ser Ala Leu Thr Ala Asp Gly Leu Ala Asn Ile Asp Ser Leu Lys
    290                 295                 300
Ile Asp Gly Asn Gln Pro Lys Ala Gly Thr Cys Ser Asn Thr Ser Ser
305                 310                 315                 320
Ser Val Ala Ser Ser Ser Ser Ser Val Lys Ser Ser Ser Ser Ser Ser
                325                 330                 335
Ser Ser Ser Ser Thr Thr Ala Lys Met Leu Thr Leu Asp Gly Asn Pro
            340                 345                 350
Ala Ala Ser Trp Phe Asn Lys Ser Arg Thr Lys Trp Asn Ser Ser Arg
        355                 360                 365
```

Ala Asp Ile Val Leu Ser Tyr Gln Gln Ala Asn Gly Gly Trp Pro Lys
370 375 380
Asn Leu Asp Tyr Asn Ser Val Ser Ala Gly Asn Gly Gly Ser Asp Ser
385 390 395 400
Gly Thr Ile Asp Asn Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala
405 410 415
Glu Val Tyr Lys Asn Gly Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg
420 425 430
Lys Ala Ala Asn Phe Ile Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu
435 440 445
Pro Gln Phe Tyr Pro Leu Lys Gly Gly Tyr Ala Asp His Ala Thr Phe
450 455 460
Asn Asp Asn Gly Met Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala Val
465 470 475 480
Asn Lys Arg Ala Pro Phe Asp Asn Asp Val Phe Ser Asp Ala Asp Arg
485 490 495
Ala Lys Phe Lys Thr Ala Val Thr Lys Gly Ile Asp Tyr Ile Leu Lys
500 505 510
Ala Gln Trp Lys Gln Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln His
515 520 525
Gly Ala Asn Asp Tyr Gln Pro Lys Ala Ala Arg Ala Tyr Glu Leu Val
530 535 540
Ser Leu Ser Gly Ser Glu Ser Val Gly Ile Ile Ala Phe Leu Met Thr
545 550 555 560
Gln Pro Gln Thr Ala Gln Ile Glu Ala Ala Val Lys Ala Gly Val Asn
565 570 575
Trp Phe Ala Ser Pro Asn Thr Tyr Leu Ala Asn Tyr Thr Tyr Asp Ser
580 585 590
Ser Lys Ala Ser Thr Asn Pro Ile Val Tyr Lys Ser Gly Ser Arg Met
595 600 605
Trp Tyr Arg Phe Tyr Asp Leu Asn Thr Asn Arg Gly Phe Phe Ser Asp
610 615 620
Arg Asp Gly Ser Lys Phe Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg
625 630 635 640
Arg Thr Gly Tyr Ser Trp Gly Gly Ser Tyr Gly Glu Ser Ile Ile Ser
645 650 655
Phe Ala Gln Lys Val Gly Tyr Leu
660

<210> 69
<211> 1035
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 69
atggcgcgtt tgttccggtg cgtgtgtgcc agcctgggag gatgggccgc ggttctggcc
60
gccgcggcgg gcccggattg gtcccgcctg ctcgcgcaac cggacccttg gtttcgcagt
120
ccggcggggc aacaggcggt gacgaacgtt ttgtcctggc agagcgcgac aggcgcctgg
180
ccgaaaaacc tggacaccac ccgcgagccg cgtcggcagg attccgcccc gcccgagggc
240
actttcgaca acggcgccac caccggcgag ttgcggtttc tggcgcgggc gtttgcggcc
300
accggcgatc cgcgctgcga agccgcggtg ctccgggggc tggacggcat cctcgcggcc
360
cagcttccca gcggcggctg gccgcagtgt catcctccgc gcgcgcctta tcagcgccac

420
atcaccttca acgacggtgt catggtgcgc atcctggagc tgctgcgcga gatagaccgc
480
gcgccggagt ttcgctgggt ggacgaggcg cggcgcgcgc gggtgcgcgc ggccttcact
540
cgcgggctgg agtgcctcct gcgctgccag gtggtcgtcg agggcagact caccgtgtgg
600
tgtgcccagc atgacgcgga gaactttcaa ccgcgaccgg cacgcgccta cgaactggaa
660
tcgctcagcg gcgcggaaag cgccggcatc ctggtgttcc tcatgagcct ggagccgcca
720
accccggaga tcgcgcgcgc ggtcgaggcc ggggcggcct ggttttcggc ggtaaagctt
780
gaagggttcc gtctcgaacg aacggccgac gacgcgcggg tggtggaaga gccgggcgcg
840
ccgccgctct gggcgcggtt ctacgagatc gggaccaatc gccccatctt tgccggtcgc
900
gacggtgtca agaagtacgc cctgagcgag atcgagcggg aacgccgggt cggctatgcg
960
tggtacggcg cctggggtga accggtcgcc cgccattatg cccagtggcg ggagcgttac
1020
gggacgcaga aatga
1035

<210> 70
<211> 344
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(22)

<221> DOMAIN
<222> (23)...(344)
<223> Catalytic domain

<400> 70
Met Ala Arg Leu Phe Arg Cys Val Cys Ala Ser Leu Gly Gly Trp Ala
 1   5   10   15
Ala Val Leu Ala Ala Ala Ala Gly Pro Asp Trp Ser Arg Leu Leu Ala
            20   25   30
Gln Pro Asp Pro Trp Phe Arg Ser Pro Ala Gly Gln Gln Ala Val Thr
        35   40   45
Asn Val Leu Ser Trp Gln Ser Ala Thr Gly Ala Trp Pro Lys Asn Leu
    50   55   60
Asp Thr Thr Arg Glu Pro Arg Arg Gln Asp Ser Ala Pro Pro Glu Gly
65   70   75   80
Thr Phe Asp Asn Gly Ala Thr Thr Gly Glu Leu Arg Phe Leu Ala Arg
                85   90   95
Ala Phe Ala Ala Thr Gly Asp Pro Arg Cys Glu Ala Ala Val Leu Arg
            100   105   110
Gly Leu Asp Gly Ile Leu Ala Ala Gln Leu Pro Ser Gly Gly Trp Pro
        115   120   125
Gln Cys His Pro Pro Arg Ala Pro Tyr Gln Arg His Ile Thr Phe Asn
    130   135   140
Asp Gly Val Met Val Arg Ile Leu Glu Leu Leu Arg Glu Ile Asp Arg
145   150   155   160
Ala Pro Glu Phe Arg Trp Val Asp Glu Ala Arg Arg Ala Arg Val Arg

```
                165                 170                 175
Ala Ala Phe Thr Arg Gly Leu Glu Cys Leu Leu Arg Cys Gln Val Val
            180                 185                 190
Val Glu Gly Arg Leu Thr Val Trp Cys Ala Gln His Asp Ala Glu Asn
        195                 200                 205
Phe Gln Pro Arg Pro Ala Arg Ala Tyr Glu Leu Glu Ser Leu Ser Gly
    210                 215                 220
Ala Glu Ser Ala Gly Ile Leu Val Phe Leu Met Ser Leu Glu Pro Pro
225                 230                 235                 240
Thr Pro Glu Ile Ala Arg Ala Val Glu Ala Gly Ala Ala Trp Phe Ser
                245                 250                 255
Ala Val Lys Leu Glu Gly Phe Arg Leu Glu Arg Thr Ala Asp Asp Ala
            260                 265                 270
Arg Val Val Glu Glu Pro Gly Ala Pro Pro Leu Trp Ala Arg Phe Tyr
        275                 280                 285
Glu Ile Gly Thr Asn Arg Pro Ile Phe Ala Gly Arg Asp Gly Val Lys
    290                 295                 300
Lys Tyr Ala Leu Ser Glu Ile Glu Arg Glu Arg Arg Val Gly Tyr Ala
305                 310                 315                 320
Trp Tyr Gly Ala Trp Gly Glu Pro Val Ala Arg His Tyr Ala Gln Trp
                325                 330                 335
Arg Glu Arg Tyr Gly Thr Gln Lys
            340
```

<210> 71
<211> 1038
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 71
gtgactcgtg tcgcccttgc gatggggctt gttgcatggg ttccggcgct cgcttcagct
60
gggcccgctg catatttgca gaagccggac gactggttcg ccagtcccga ggccagggca
120
atcgccgcga acgtactcgc gcatcaggcc gatctcggcg ggtggccgaa gaacatcgac
180
acaacgaagc cgttcaccgg cgaccggacg caaatcaaac cgaccttcga taacagcgcg
240
acaaccgacg agctccggtt tctggcgcgc atccacaacg cgactcgcga cgagaagtac
300
cgcaccgcgt tcgagaaggg gctcgattac atcttgaaag cacaatacgc aaacggcggt
360
tggccgcagt cgcacccgcc cggcaccggc taccaccggc acatcacctt caacgacaat
420
gccatggtcc gtttgatgga gctcgtgcgc gaagtcgcga cctcgaatcg gtacgacttc
480
ctggacgccg accgccgcaa ggcctgccgc gccgctttcg atcgcggcat cgaatgcatc
540
ctgaagtgcc agatcaaggt cgacagtaag ctgacggcat ggtgcgccca gcacgacgag
600
aaggacctcg ctccccggcc ggcgcggacc tacgagctcg tctcactcag cggctcggag
660
tcggtcggga tcgtccgcct actcatgagc ctcgatcgac caagcccgga ggtcgctcgg
720
gccatcgacg gcgcggtcgc gtggttccag tcggcgaagc tcgaaggcac caaggtcgtt
780
gtcgagcgcg acccgaagta tccgggcggc cgggaacgcg tggtggtgaa ggatccaaag
840

gcaccgccac tctgggcgcg cttctacgaa atcggcacga atcgccccat cttctccgac
900
cgcgacggca tcaagaagta cgcgctcgcc gagatcggcc ccgaacggcg gaatggctat
960
gcctggtatg gcacctggcc gcgcgacctg ctggagaagg aatacccagg gtggaaaaag
1020
aagctggccc ggccgtga
1038

<210> 72
<211> 345
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(20)

<221> DOMAIN
<222> (21)...(345)
<223> Catalytic domain

<400> 72
Met Thr Arg Val Ala Leu Ala Met Gly Leu Val Ala Trp Val Pro Ala
 1   5   10   15
Leu Ala Ser Ala Gly Pro Ala Ala Tyr Leu Gln Lys Pro Asp Asp Trp
            20   25   30
Phe Ala Ser Pro Glu Ala Arg Ala Ile Ala Ala Asn Val Leu Ala His
        35   40   45
Gln Ala Asp Leu Gly Gly Trp Pro Lys Asn Ile Asp Thr Thr Lys Pro
    50   55   60
Phe Thr Gly Asp Arg Thr Gln Ile Lys Pro Thr Phe Asp Asn Ser Ala
65   70   75   80
Thr Thr Asp Glu Leu Arg Phe Leu Ala Arg Ile His Asn Ala Thr Arg
                85   90   95
Asp Glu Lys Tyr Arg Thr Ala Phe Glu Lys Gly Leu Asp Tyr Ile Leu
            100   105   110
Lys Ala Gln Tyr Ala Asn Gly Gly Trp Pro Gln Ser His Pro Pro Gly
        115   120   125
Thr Gly Tyr His Arg His Ile Thr Phe Asn Asp Asn Ala Met Val Arg
    130   135   140
Leu Met Glu Leu Val Arg Glu Val Ala Thr Ser Asn Arg Tyr Asp Phe
145   150   155   160
Leu Asp Ala Asp Arg Arg Lys Ala Cys Arg Ala Ala Phe Asp Arg Gly
                165   170   175
Ile Glu Cys Ile Leu Lys Cys Gln Ile Lys Val Asp Ser Lys Leu Thr
            180   185   190
Ala Trp Cys Ala Gln His Asp Glu Lys Asp Leu Ala Pro Arg Pro Ala
        195   200   205
Arg Thr Tyr Glu Leu Val Ser Leu Ser Gly Ser Glu Ser Val Gly Ile
    210   215   220
Val Arg Leu Leu Met Ser Leu Asp Arg Pro Ser Pro Glu Val Ala Arg
225   230   235   240
Ala Ile Asp Gly Ala Val Ala Trp Phe Gln Ser Ala Lys Leu Glu Gly
                245   250   255
Thr Lys Val Val Val Glu Arg Asp Pro Lys Tyr Pro Gly Gly Arg Glu
            260   265   270
Arg Val Val Val Lys Asp Pro Lys Ala Pro Pro Leu Trp Ala Arg Phe
        275   280   285

Tyr Glu Ile Gly Thr Asn Arg Pro Ile Phe Ser Asp Arg Asp Gly Ile
290 295 300
Lys Lys Tyr Ala Leu Ala Glu Ile Gly Pro Glu Arg Arg Asn Gly Tyr
305 310 315 320
Ala Trp Tyr Gly Thr Trp Pro Arg Asp Leu Leu Glu Lys Glu Tyr Pro
325 330 335
Gly Trp Lys Lys Lys Leu Ala Arg Pro
340 345

<210> 73
<211> 1221
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 73
atgctcacca aaacatcact acttattgca ttgctaggca gttgttgtat cgcaccatta
60
catgcggaca caccagcaag caatgcaccg acaaccaatg catcaattcc gctacagcaa
120
actgcgagcg atgctgccgc ctggaaaaat tatctcgcca aatccaacga gttgcgcaaa
180
gcagaccagg cgcagctcaa agccgagctg aaaaaactcg ggcaaaaaac cgcgagtttg
240
cctgagtaca ccaaagaatt tggttttgaa gtgaagcagt catctgagtg gtttaaaagc
300
actgaaggta aacgagtgat ggatattatc ctatcgtttc aaactccttc tggcggctgg
360
tcaaaacgca ctgacatgag caaagcgccg cgcaaacccg gccaggcatt tggtgttgaa
420
aaaaattaca tccccacctt tgataatggc gcgaccagca cacaattaat gctactggca
480
caggcgcatc aagccactgg cgataaacgc tacagcgatg catttgcgcg cgggcttgaa
540
tttatcatca ccgctcaata tcccaatggc ggctggccac aaaattttcc attggttggc
600
aagtatcacg atcacatcac ttacaacgat gccctgatgc gcgatttaat ggtagtgcta
660
cacaaggttg ccatggccaa ggatgaattt gcctttgtat ccaaggcgca gcaacaggcc
720
gcacaagcga gcctcgaacg cgcgctggac tgcgttttga aaacccaggt gatggccaat
780
ggccaattaa ctatatgggg tgcgcagcac gatgccaaaa ccttaaaacc cgccaaagcg
840
cgcgcctatg aaatgatttc actcaccagt tctgaaagcg tgtggatgct cgatttttta
900
atggatttgc aacagcccag cgctgacatt attaaatccg tgcacgcggc tgccgcttgg
960
tatgagcaaa ataaaattat cggaaaaacc tggacccggg gcgacacagt tctgaaagac
1020
gataaggatg caccgccaat ctgggcgcgt ttttatgaga taggtacgaa caaacccctg
1080
tttggcgacc gcgatgactc tgtccattac gatctggcaa aggtatcgga agagcgccgc
1140
acgggttatg cctggtacac aacctcaccc aatcaggtat taaaaaagta cgcgcgctgg
1200
gctaaacaat atccgcaata a
1221

<210> 74
<211> 406
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(22)

<221> DOMAIN
<222> (23)...(406)
<223> Catalytic domain

<400> 74
Met Leu Thr Lys Thr Ser Leu Leu Ile Ala Leu Leu Gly Ser Cys Cys
 1   5   10   15
Ile Ala Pro Leu His Ala Asp Thr Pro Ala Ser Asn Ala Pro Thr Thr
            20   25   30
Asn Ala Ser Ile Pro Leu Gln Gln Thr Ala Ser Asp Ala Ala Ala Trp
        35   40   45
Lys Asn Tyr Leu Ala Lys Ser Asn Glu Leu Arg Lys Ala Asp Gln Ala
    50   55   60
Gln Leu Lys Ala Glu Leu Lys Lys Leu Gly Gln Lys Thr Ala Ser Leu
65   70   75   80
Pro Glu Tyr Thr Lys Glu Phe Gly Phe Glu Val Lys Gln Ser Ser Glu
                85   90   95
Trp Phe Lys Ser Thr Glu Gly Lys Arg Val Met Asp Ile Ile Leu Ser
            100   105   110
Phe Gln Thr Pro Ser Gly Gly Trp Ser Lys Arg Thr Asp Met Ser Lys
        115   120   125
Ala Pro Arg Lys Pro Gly Gln Ala Phe Gly Val Glu Lys Asn Tyr Ile
    130   135   140
Pro Thr Phe Asp Asn Gly Ala Thr Ser Thr Gln Leu Met Leu Leu Ala
145   150   155   160
Gln Ala His Gln Ala Thr Gly Asp Lys Arg Tyr Ser Asp Ala Phe Ala
                165   170   175
Arg Gly Leu Glu Phe Ile Ile Thr Ala Gln Tyr Pro Asn Gly Gly Trp
            180   185   190
Pro Gln Asn Phe Pro Leu Val Gly Lys Tyr His Asp His Ile Thr Tyr
        195   200   205
Asn Asp Ala Leu Met Arg Asp Leu Met Val Val Leu His Lys Val Ala
    210   215   220
Met Ala Lys Asp Glu Phe Ala Phe Val Ser Lys Ala Gln Gln Gln Ala
225   230   235   240
Ala Gln Ala Ser Leu Glu Arg Ala Leu Asp Cys Val Leu Lys Thr Gln
                245   250   255
Val Met Ala Asn Gly Gln Leu Thr Ile Trp Gly Ala Gln His Asp Ala
            260   265   270
Lys Thr Leu Lys Pro Ala Lys Ala Arg Ala Tyr Glu Met Ile Ser Leu
        275   280   285
Thr Ser Ser Glu Ser Val Trp Met Leu Asp Phe Leu Met Asp Leu Gln
    290   295   300
Gln Pro Ser Ala Asp Ile Ile Lys Ser Val His Ala Ala Ala Ala Trp
305   310   315   320
Tyr Glu Gln Asn Lys Ile Ile Gly Lys Thr Trp Thr Arg Gly Asp Thr
                325   330   335
Val Leu Lys Asp Asp Lys Asp Ala Pro Pro Ile Trp Ala Arg Phe Tyr
            340   345   350
Glu Ile Gly Thr Asn Lys Pro Leu Phe Gly Asp Arg Asp Asp Ser Val

355 360 365
His Tyr Asp Leu Ala Lys Val Ser Glu Glu Arg Arg Thr Gly Tyr Ala
370 375 380
Trp Tyr Thr Thr Ser Pro Asn Gln Val Leu Lys Lys Tyr Ala Arg Trp
385 390 395 400
Ala Lys Gln Tyr Pro Gln
405

<210> 75
<211> 1767
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 75
atgaccacaa cccgccgcac tatcctgaaa gccgccgcca gcgccggcgc gatcgccagc
60
accggctggc ccgccttggc cgccgcacag gccgcgcaag ccgccgaccc gtgggcccgc
120
gcccagcaga tcatcgaccg cttcgccaag ccgctcagct tcccgaacag ggacttcccg
180
atcaccgagt tcggcgccaa accctgcaag ctggtcaaag cccagggcct ggtcgaagta
240
agagtcaaag gcgaactcga aacgccagca ccgcaagcgc cggacgccta cccggcaatc
300
aaagccgcca tcgccgcagc gagcaaggcc ggaggagggc gcgtgctgat cccggccggc
360
aactggtact gcaagggccc tatcgtgctg ctgtcgaacg tgcacgtgca ccttgccaag
420
ggcgcgcaag tctacttcag cgccaacgcc aaggacttcg cccgcgacgg cgactacgac
480
tgcggcgcca acggcaagct ggtgctctcg cgctggcaag gcaacgattg cctgaacttc
540
tcgcccatgg tctacgcgcg cgggcaaaag aatatcgcca ttaccggcga agactggacc
600
agcatcctga acggccaggc cggcgtggcg ttcgaagacg gcagcggcaa tggctggtgg
660
ggcatgaacc ccgccggcgc gccgcccggc agcaccacgc accagggcgc agccaatccg
720
aacaacgccg aggagccaat cgccagactg cccacgcgcc acgcgaactg gagcgccgac
780
gacaagtacc tgccgctgct gtccgaagcc ggcgtgcccg ccgagcgccg cgtgttcggt
840
ctggggcact acctgcggcc gtcgatggtc gaattcgtcg actgcgggga tgtgctgatg
900
cagggctacc aggtcatcaa cacgccgttc tggattcatc acccggtcaa ctcacgcaac
960
attcacttct ccaaagtgcg catggaaagc atcggcccga attcggacgg tttcgatccc
1020
gagtcctgcg acaccatcct ggtggacggc tgcctgttca ataccggcga cgactgcatc
1080
gccatcaaat ccggcaagaa ccgagactcg caatacggcc caacgcgcaa tatggtggtc
1140
cagaactgca tcatgaaccg cggccacggc ggcgttacgc tgggcagcga aatggcgggt
1200
ggcatcgagc atatctacgc gcagaaaatc gaattccgca acgcgttctg ggaccacgac
1260
ccgctgggca cggccatccg aatgaagacg aacatgaacc gcggcggcta ccttcgtcat
1320

ttctacgtgc gcgacgtgac gctgccgaat ggcgtgcgta ccaagagcgg cttctacaag
1380
acgctgccgg gatctccgct ggcaggcaag gtctccacca gcggcggcgc tgttatcact
1440
atcgactgcg attacgcgcc gaatgacgac agcgtgcgcg tgcggccgcc gcaggtgtcg
1500
gacgtgcata tctcgaacgt ccgcgtcagc aatgtgaaaa cggccgaagg ctcgttctcc
1560
tgctaccagg ccatggtgct gctcgggccc gtggcggcca gcttcaacgg cgcgcctggc
1620
acggccatcc tgccgatcac gaatgtcacc gtcagcgatt cggacttcgg cacgccgcgc
1680
aacagcgcag agccctggtt cgcgttcaac gtgcagggac tcaagctgcg caacgtgcgc
1740
atcgatggca aggagtacaa cgtatga
1767

<210> 76
<211> 588
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(34)

<221> DOMAIN
<222> (110)...(555)
<223> Catalytic domain

<400> 76
Met Thr Thr Thr Arg Arg Thr Ile Leu Lys Ala Ala Ala Ser Ala Gly
 1   5   10   15
Ala Ile Ala Ser Thr Gly Trp Pro Ala Leu Ala Ala Ala Gln Ala Ala
            20   25   30
Gln Ala Ala Asp Pro Trp Ala Arg Ala Gln Gln Ile Ile Asp Arg Phe
        35   40   45
Ala Lys Pro Leu Ser Phe Pro Asn Arg Asp Phe Pro Ile Thr Glu Phe
    50   55   60
Gly Ala Lys Pro Cys Lys Leu Val Lys Ala Gln Gly Leu Val Glu Val
65   70   75   80
Arg Val Lys Gly Glu Leu Glu Thr Pro Ala Pro Gln Ala Pro Asp Ala
                85   90   95
Tyr Pro Ala Ile Lys Ala Ala Ile Ala Ala Ala Ser Lys Ala Gly Gly
            100   105   110
Gly Arg Val Leu Ile Pro Ala Gly Asn Trp Tyr Cys Lys Gly Pro Ile
        115   120   125
Val Leu Leu Ser Asn Val His Val His Leu Ala Lys Gly Ala Gln Val
    130   135   140
Tyr Phe Ser Ala Asn Ala Lys Asp Phe Ala Arg Asp Gly Asp Tyr Asp
145   150   155   160
Cys Gly Ala Asn Gly Lys Leu Val Leu Ser Arg Trp Gln Gly Asn Asp
                165   170   175
Cys Leu Asn Phe Ser Pro Met Val Tyr Ala Arg Gly Gln Lys Asn Ile
            180   185   190
Ala Ile Thr Gly Glu Asp Trp Thr Ser Ile Leu Asn Gly Gln Ala Gly
        195   200   205
Val Ala Phe Glu Asp Gly Ser Gly Asn Gly Trp Trp Gly Met Asn Pro
    210   215   220

```
Ala Gly Ala Pro Pro Gly Ser Thr Thr His Gln Gly Ala Ala Asn Pro
225                 230                 235                 240
Asn Asn Ala Glu Glu Pro Ile Ala Arg Leu Pro Thr Arg His Ala Asn
                245                 250                 255
Trp Ser Ala Asp Asp Lys Tyr Leu Pro Leu Leu Ser Glu Ala Gly Val
            260                 265                 270
Pro Ala Glu Arg Arg Val Phe Gly Leu Gly His Tyr Leu Arg Pro Ser
        275                 280                 285
Met Val Glu Phe Val Asp Cys Gly Asp Val Leu Met Gln Gly Tyr Gln
    290                 295                 300
Val Ile Asn Thr Pro Phe Trp Ile His His Pro Val Asn Ser Arg Asn
305                 310                 315                 320
Ile His Phe Ser Lys Val Arg Met Glu Ser Ile Gly Pro Asn Ser Asp
                325                 330                 335
Gly Phe Asp Pro Glu Ser Cys Asp Thr Ile Leu Val Asp Gly Cys Leu
            340                 345                 350
Phe Asn Thr Gly Asp Asp Cys Ile Ala Ile Lys Ser Gly Lys Asn Arg
        355                 360                 365
Asp Ser Gln Tyr Gly Pro Thr Arg Asn Met Val Val Gln Asn Cys Ile
    370                 375                 380
Met Asn Arg Gly His Gly Gly Val Thr Leu Gly Ser Glu Met Ala Gly
385                 390                 395                 400
Gly Ile Glu His Ile Tyr Ala Gln Lys Ile Glu Phe Arg Asn Ala Phe
                405                 410                 415
Trp Asp His Asp Pro Leu Gly Thr Ala Ile Arg Met Lys Thr Asn Met
            420                 425                 430
Asn Arg Gly Gly Tyr Leu Arg His Phe Tyr Val Arg Asp Val Thr Leu
        435                 440                 445
Pro Asn Gly Val Arg Thr Lys Ser Gly Phe Tyr Lys Thr Leu Pro Gly
    450                 455                 460
Ser Pro Leu Ala Gly Lys Val Ser Thr Ser Gly Gly Ala Val Ile Thr
465                 470                 475                 480
Ile Asp Cys Asp Tyr Ala Pro Asn Asp Asp Ser Val Arg Val Arg Pro
                485                 490                 495
Pro Gln Val Ser Asp Val His Ile Ser Asn Val Arg Val Ser Asn Val
            500                 505                 510
Lys Thr Ala Glu Gly Ser Phe Ser Cys Tyr Gln Ala Met Val Leu Leu
        515                 520                 525
Gly Pro Val Ala Ala Ser Phe Asn Gly Ala Pro Gly Thr Ala Ile Leu
    530                 535                 540
Pro Ile Thr Asn Val Thr Val Ser Asp Ser Asp Phe Gly Thr Pro Arg
545                 550                 555                 560
Asn Ser Ala Glu Pro Trp Phe Ala Phe Asn Val Gln Gly Leu Lys Leu
                565                 570                 575
Arg Asn Val Arg Ile Asp Gly Lys Glu Tyr Asn Val
            580                 585
```

<210> 77
<211> 2043
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 77
atgaaaacct ccagagcaat ttttactaca tcaacacttt tacaccgcgc gcttatcgcg
60
gctagtgtca gcatggcaat gagttctgcc gcatgggcgg gttgtaccta taccgtcacc
120
aataattggg gctcaggatt taccggcgaa atcaaagtga ccaacaacac caccgccagc

180
gtgaacaatt ggtctgtgtc atggcaggaa tccggtgcgg ctatcaccaa cgcctggaat
240
gcaacgctca gtggctcaaa cccttacaca gccgtatccg ctggttggaa tggcacactt
300
gcccccaatg catcggccac ttttggtttc caggcaaacg gttctgccgg tgcacctaaa
360
gtgaatggca gcttgtgcgg caccaacact tcatcaacac cggcatccag cagtgttgcc
420
agctcggtta aatcaagcgc gcccgtatcg tccagcagca gatcatccag ttcaatcgct
480
atcactagca gctctttagc gagaagttct attgcctcca gcagctcact agttagtagc
540
tccagagcga gcagtagtgc gccaagcgtt ttctctttta cgatccagga agagcaagcg
600
ggcttctgtc gtgttgatgg cattgcgaca gaaagcacca acaccggttt taccggcaat
660
ggctacacca atgcgaacaa cgcgcaaggc gcagcgattg aatgggcagt cagcgcacct
720
agcagtggcc gttatacagt agccttccgc ttcgccaatg gcggcacagc agcgcgcaac
780
ggctcgttgt taatcaatgg cggtagcaat ggtaattaca ctgtggagtt acccctgacc
840
ggcgcatggg caacctggca aattgccagc gtggaaattg atttagtgca aggcaataat
900
attttaaaac tctcggcgtt aaccgctgac ggtttggcca atatcgactc attaaaaata
960
gacggcgcgc aaaccaaagc aggtacttgc agcactacat caagcagcag cgttgccagc
1020
agctcgtcgt ccgttaaatc cagcgcaagt tcttcttcga gttcatccac cgctgcaaaa
1080
atactgacat tagacggtaa cccggccgcc agctggttca acaaatccag gaccaagtgg
1140
aatagcagcc gcgccgatat tgtgttgtct taccagcaat ccaacggcgg ttggccaaaa
1200
aacctggatt acaactcagt gagcgcaggc aatggcggga gcgacagcgg caccatcgac
1260
aatggtgcaa ccattaccga aatggtttac ctcgctgaaa tttataaaaa cggcggcaac
1320
accaaatatc gcgatgcagt gcgcagagca gcaaactttt tagtgagctc gcaatacagc
1380
acaggcgcct tgccacaatt ttatccgttg aaaggcggct atgcggatca tgcgaccttt
1440
aacgataacg gcatggcgta cgcgttgacg gtattggatt tcgcagtaaa caaacgcgca
1500
ccgtttgata acgacatttt ctctgattct gatcgggcga aattcaaaac cgctgttgcc
1560
aaaggtgtgg attacatttt aaaagcgcag tggaaacaaa atggaaaact cactgcatgg
1620
tgtgcacaac acggtgctac ggattaccaa ccgaaaaaag cgcgcgctta tgaattggaa
1680
tcattgagtg gtagcgagtc ggtcggcatt ctcgccttct tgatgaccca accacaaacc
1740
gcgcaaatcg aagcggcggt caaggcgggt gtcaactggt tcgccagtcc aaatacttat
1800
ttggctaact acacttacga ttcatcaaaa gcgtctacca acccgattgt gtataaatcc
1860
ggaagcagaa tgtggtatcg cttctatgac ctgaacacca accgtggttt ctttagtgat
1920
cgcgatggca gcaaattcta tgatatcacc caaatgtcag aagagcgtcg caccggttat
1980

agctggggtg gctcttacgg tgaatctatt atttccttcg cgcaaaaagt gggttatctg
2040
taa
2043

<210> 78
<211> 680
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(33)

<221> BINDING
<222> (34)...(126)
<223> Carbohydrate binding module

<221> BINDING
<222> (199)...(322)
<223> Carbohydrate binding module

<221> DOMAIN
<222> (323)...(680)
<223> Catalytic domain

<400> 78
Met Lys Thr Ser Arg Ala Ile Phe Thr Thr Ser Thr Leu Leu His Arg
 1   5   10   15
Ala Leu Ile Ala Ala Ser Val Ser Met Ala Met Ser Ser Ala Ala Trp
            20   25   30
Ala Gly Cys Thr Tyr Thr Val Thr Asn Asn Trp Gly Ser Gly Phe Thr
        35   40   45
Gly Glu Ile Lys Val Thr Asn Asn Thr Thr Ala Ser Val Asn Asn Trp
    50   55   60
Ser Val Ser Trp Gln Glu Ser Gly Ala Ala Ile Thr Asn Ala Trp Asn
65   70   75   80
Ala Thr Leu Ser Gly Ser Asn Pro Tyr Thr Ala Val Ser Ala Gly Trp
                85   90   95
Asn Gly Thr Leu Ala Pro Asn Ala Ser Ala Thr Phe Gly Phe Gln Ala
            100   105   110
Asn Gly Ser Ala Gly Ala Pro Lys Val Asn Gly Ser Leu Cys Gly Thr
        115   120   125
Asn Thr Ser Ser Thr Pro Ala Ser Ser Ser Val Ala Ser Ser Val Lys
    130   135   140
Ser Ser Ala Pro Val Ser Ser Ser Ser Arg Ser Ser Ser Ser Ile Ala
145   150   155   160
Ile Thr Ser Ser Ser Leu Ala Arg Ser Ser Ile Ala Ser Ser Ser Ser
                165   170   175
Leu Val Ser Ser Ser Arg Ala Ser Ser Ser Ala Pro Ser Val Phe Ser
            180   185   190
Phe Thr Ile Gln Glu Glu Gln Ala Gly Phe Cys Arg Val Asp Gly Ile
        195   200   205
Ala Thr Glu Ser Thr Asn Thr Gly Phe Thr Gly Asn Gly Tyr Thr Asn
    210   215   220
Ala Asn Asn Ala Gln Gly Ala Ala Ile Glu Trp Ala Val Ser Ala Pro
225   230   235   240
Ser Ser Gly Arg Tyr Thr Val Ala Phe Arg Phe Ala Asn Gly Gly Thr
                245   250   255

```
Ala Ala Arg Asn Gly Ser Leu Leu Ile Asn Gly Gly Ser Asn Gly Asn
            260                 265                 270
Tyr Thr Val Glu Leu Pro Leu Thr Gly Ala Trp Ala Thr Trp Gln Ile
        275                 280                 285
Ala Ser Val Glu Ile Asp Leu Val Gln Gly Asn Asn Ile Leu Lys Leu
    290                 295                 300
Ser Ala Leu Thr Ala Asp Gly Leu Ala Asn Ile Asp Ser Leu Lys Ile
305                 310                 315                 320
Asp Gly Ala Gln Thr Lys Ala Gly Thr Cys Ser Thr Thr Ser Ser Ser
                325                 330                 335
Ser Val Ala Ser Ser Ser Ser Ser Val Lys Ser Ser Ala Ser Ser Ser
            340                 345                 350
Ser Ser Ser Ser Thr Ala Ala Lys Ile Leu Thr Leu Asp Gly Asn Pro
        355                 360                 365
Ala Ala Ser Trp Phe Asn Lys Ser Arg Thr Lys Trp Asn Ser Ser Arg
    370                 375                 380
Ala Asp Ile Val Leu Ser Tyr Gln Gln Ser Asn Gly Gly Trp Pro Lys
385                 390                 395                 400
Asn Leu Asp Tyr Asn Ser Val Ser Ala Gly Asn Gly Gly Ser Asp Ser
                405                 410                 415
Gly Thr Ile Asp Asn Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala
            420                 425                 430
Glu Ile Tyr Lys Asn Gly Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg
        435                 440                 445
Arg Ala Ala Asn Phe Leu Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu
    450                 455                 460
Pro Gln Phe Tyr Pro Leu Lys Gly Gly Tyr Ala Asp His Ala Thr Phe
465                 470                 475                 480
Asn Asp Asn Gly Met Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala Val
                485                 490                 495
Asn Lys Arg Ala Pro Phe Asp Asn Asp Ile Phe Ser Asp Ser Asp Arg
            500                 505                 510
Ala Lys Phe Lys Thr Ala Val Ala Lys Gly Val Asp Tyr Ile Leu Lys
        515                 520                 525
Ala Gln Trp Lys Gln Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln His
    530                 535                 540
Gly Ala Thr Asp Tyr Gln Pro Lys Lys Ala Arg Ala Tyr Glu Leu Glu
545                 550                 555                 560
Ser Leu Ser Gly Ser Glu Ser Val Gly Ile Leu Ala Phe Leu Met Thr
                565                 570                 575
Gln Pro Gln Thr Ala Gln Ile Glu Ala Ala Val Lys Ala Gly Val Asn
            580                 585                 590
Trp Phe Ala Ser Pro Asn Thr Tyr Leu Ala Asn Tyr Thr Tyr Asp Ser
        595                 600                 605
Ser Lys Ala Ser Thr Asn Pro Ile Val Tyr Lys Ser Gly Ser Arg Met
    610                 615                 620
Trp Tyr Arg Phe Tyr Asp Leu Asn Thr Asn Arg Gly Phe Phe Ser Asp
625                 630                 635                 640
Arg Asp Gly Ser Lys Phe Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg
                645                 650                 655
Arg Thr Gly Tyr Ser Trp Gly Gly Ser Tyr Gly Glu Ser Ile Ile Ser
            660                 665                 670
Phe Ala Gln Lys Val Gly Tyr Leu
        675                 680
```

<210> 79
<211> 1746
<212> DNA
<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 79
atgacgacac gacgcgaatt catcaaaggc tttctactta ccggagcagc cgtggccgtc
60
gctccgcgtt taattgcgtt cggcgcggag gcaagtccgt gggaaacgat gatgccttcg
120
atcctcgcac gcatcacacc acctcgtttt ccgaaacgca ccttctatct caatcgattc
180
ggcgccaagg gcgatggagt cacagactgc accgcggctt ttcatcgcgc gatcgatgaa
240
tgcaccaaag ccggcggtgg gaaagtcgtc gtgccggcgg gcacttatct caccggcgcg
300
attcatttga agagcaacgt caacctcgaa gtctcggaag gcgcgacgat caagttcagt
360
caggacccga aacactacct gcctgttgtc ttctcgcgtt gggaaggtgt cgaagtcttc
420
aactactcgc ctttcattta cgcgttcgaa cagcgaaaca tcgcgatcac cggcaaaggc
480
acgctcgacg gacagagtga ttcggaacac tggtggccgt ggaacggccg tccgcagtac
540
ggatggaatg aagggatgaa acagcagcgt cccgatcgca acgcgttgtt cacaatggcg
600
gagaaaggcg tgccggtgcg cgagcgcatc tttggcgaag gtcattattt gaggccgcag
660
ttcattcagc cgtaccgctg ccagaacgtg ctgatccagg gcgtgacgat tcggaactcg
720
ccgatgtggg agattcatcc ggtgttgtgc cgcaacgtga ctattcacga cgtgcacatc
780
gatagtcatg gaccaaacaa cgacggctgc aatcccgaat cgtgcagcga cgtgttgatt
840
aaggatagct acttcgatac cggcgacgac tgcatcgcga tcaaatcggg acgcaacgcc
900
gacgggcggc ggcttaaagc gccgactgag aacatcatcg ttcaaggatg tcgcatgaaa
960
gacggccacg gtggaatcac ggtcggcagc gagatctcgg gcggcgtgcg aaacctgttt
1020
gccgagaatt gccggctcga cagtccaaac ctcgatcacg ccctgcgcgt gaagaacaat
1080
gccatgcgcg gcggattact cgagaacttc cacttccgta acatcgaagt cgggcaggtg
1140
gcccatgccg tgattacgat cgacttcaac tacgaagagg gcgcgaaagg gtcgttcacg
1200
ccggtcgttc gcgattacac ggtcgatcgt ttgcgcagca cgaagagcaa gcacgcactc
1260
gacgtccagg gtctgcccgg cgcgccggtc atcaacctgc gattgacaaa ctgcacattc
1320
aacgatgtgc agcaaccgaa cattctcaag aacgtcgaac aatcaacctt tgagaacgtc
1380
acgattaacg gaaagacgat cacacaaaca ggatccatct cagaaagagc ggccacgaca
1440
gcaatgaccg cgctttggcg cgacgcgtcg aggaaagaaa acggttatcc cgcgaagtgg
1500
acctatgatc atgggctggt cctgaaagga atcgagcgcg tttggaacaa taccggcgat
1560
aagaagtatc tgaagttcat ccaggacagc atggaccact tcgtcaacga cgacggctcc
1620
attcgcacct acacgatcga cgagtacaac atcgatcacg ttcttcccgg acgaaacctc
1680
ctgttccttt acaaaactac cggtcaggaa aagtatcgca aagccgccgc gttcttgcgc
1740

gaacaa
1746

<210> 80
<211> 582
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(28)

<221> DOMAIN
<222> (81)...(458)
<223> Catalytic domain

<400> 80

```
Met Thr Thr Arg Arg Glu Phe Ile Lys Gly Phe Leu Leu Thr Gly Ala
 1               5                  10                  15
Ala Val Ala Val Ala Pro Arg Leu Ile Ala Phe Gly Ala Glu Ala Ser
            20                  25                  30
Pro Trp Glu Thr Met Met Pro Ser Ile Leu Ala Arg Ile Thr Pro Pro
        35                  40                  45
Arg Phe Pro Lys Arg Thr Phe Tyr Leu Asn Arg Phe Gly Ala Lys Gly
    50                  55                  60
Asp Gly Val Thr Asp Cys Thr Ala Ala Phe His Arg Ala Ile Asp Glu
65                  70                  75                  80
Cys Thr Lys Ala Gly Gly Gly Lys Val Val Val Pro Ala Gly Thr Tyr
                85                  90                  95
Leu Thr Gly Ala Ile His Leu Lys Ser Asn Val Asn Leu Glu Val Ser
            100                 105                 110
Glu Gly Ala Thr Ile Lys Phe Ser Gln Asp Pro Lys His Tyr Leu Pro
        115                 120                 125
Val Val Phe Ser Arg Trp Glu Gly Val Glu Val Phe Asn Tyr Ser Pro
    130                 135                 140
Phe Ile Tyr Ala Phe Glu Gln Arg Asn Ile Ala Ile Thr Gly Lys Gly
145                 150                 155                 160
Thr Leu Asp Gly Gln Ser Asp Ser Glu His Trp Trp Pro Trp Asn Gly
                165                 170                 175
Arg Pro Gln Tyr Gly Trp Asn Glu Gly Met Lys Gln Gln Arg Pro Asp
            180                 185                 190
Arg Asn Ala Leu Phe Thr Met Ala Glu Lys Gly Val Pro Val Arg Glu
        195                 200                 205
Arg Ile Phe Gly Glu Gly His Tyr Leu Arg Pro Gln Phe Ile Gln Pro
    210                 215                 220
Tyr Arg Cys Gln Asn Val Leu Ile Gln Gly Val Thr Ile Arg Asn Ser
225                 230                 235                 240
Pro Met Trp Glu Ile His Pro Val Leu Cys Arg Asn Val Thr Ile His
                245                 250                 255
Asp Val His Ile Asp Ser His Gly Pro Asn Asn Asp Gly Cys Asn Pro
            260                 265                 270
Glu Ser Cys Ser Asp Val Leu Ile Lys Asp Ser Tyr Phe Asp Thr Gly
        275                 280                 285
Asp Asp Cys Ile Ala Ile Lys Ser Gly Arg Asn Ala Asp Gly Arg Arg
    290                 295                 300
Leu Lys Ala Pro Thr Glu Asn Ile Ile Val Gln Gly Cys Arg Met Lys
305                 310                 315                 320
Asp Gly His Gly Gly Ile Thr Val Gly Ser Glu Ile Ser Gly Gly Val
                325                 330                 335
```

Arg Asn Leu Phe Ala Glu Asn Cys Arg Leu Asp Ser Pro Asn Leu Asp
340 345 350
His Ala Leu Arg Val Lys Asn Asn Ala Met Arg Gly Gly Leu Leu Glu
355 360 365
Asn Phe His Phe Arg Asn Ile Glu Val Gly Gln Val Ala His Ala Val
370 375 380
Ile Thr Ile Asp Phe Asn Tyr Glu Glu Gly Ala Lys Gly Ser Phe Thr
385 390 395 400
Pro Val Val Arg Asp Tyr Thr Val Asp Arg Leu Arg Ser Thr Lys Ser
405 410 415
Lys His Ala Leu Asp Val Gln Gly Leu Pro Gly Ala Pro Val Ile Asn
420 425 430
Leu Arg Leu Thr Asn Cys Thr Phe Asn Asp Val Gln Gln Pro Asn Ile
435 440 445
Leu Lys Asn Val Glu Gln Ser Thr Phe Glu Asn Val Thr Ile Asn Gly
450 455 460
Lys Thr Ile Thr Gln Thr Gly Ser Ile Ser Glu Arg Ala Ala Thr Thr
465 470 475 480
Ala Met Thr Ala Leu Trp Arg Asp Ala Ser Arg Lys Glu Asn Gly Tyr
485 490 495
Pro Ala Lys Trp Thr Tyr Asp His Gly Leu Val Leu Lys Gly Ile Glu
500 505 510
Arg Val Trp Asn Asn Thr Gly Asp Lys Lys Tyr Leu Lys Phe Ile Gln
515 520 525
Asp Ser Met Asp His Phe Val Asn Asp Asp Gly Ser Ile Arg Thr Tyr
530 535 540
Thr Ile Asp Glu Tyr Asn Ile Asp His Val Leu Pro Gly Arg Asn Leu
545 550 555 560
Leu Phe Leu Tyr Lys Thr Thr Gly Gln Glu Lys Tyr Arg Lys Ala Ala
565 570 575
Ala Phe Leu Arg Glu Gln
580

<210> 81
<211> 1065
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 81
atgacgctac ccgttgtttc cctgcgcgtg ctgctggcgc tgctggccac gttgccggtc
60
gcctgcgcgg gcgctgcggt atccgcggca gcgaccgacc cggtcgccga gaacatgctg
120
ctgctgcaga ccgcctccgg tggctggtcc aagcactacc gcgggaagaa ggtcgactac
180
acgcgcaatt acgacaccgc cgagcgcgcc gcgctgcgcg cgcccggccg gcatgacgac
240
gcgacgatcg acaacaaggc cacgaccagc gagatcgcct acctggtgca ggcacatgcc
300
aggacgggca acccggcgta cctcgacggt gcccgccgcg gggtcgaata cctgctgcgc
360
gcgcagtacc cgaatggtgg ctggccgcag ttctaccccg accactcgtc ctaccggcac
420
cagatcacgc tcaacgacga cgcgatggtg catgccatca ccgtgctgca ggacatcgcc
480
gccggccgcg acggcatgca ggcgttgacg cccgagttcg gcgtccgcgc cgccgccgcc
540
gcgcagcgcg gcatcggaaa cctgctcgag ttgcaggtgc ggatcgacgg cgagccgacc

600
atctgggccg cgcagtacga cgagcatagc ctgcagccgg ccaaggcccg cgcctatgaa
660
ctgccctcgc tggccgtggc cgaatcggtc ggcgtggtgc gcctgctgat gcgccagccg
720
aggccggatg cccggaccgt cgccgcgatc gaatcggcgg cccgctggct ggaggcgcat
780
cgcctgcatg acctggcgct cgaacgcgtc gacgcaccgg ccgaggaaac gggcaaggac
840
gtgcgggtcg tgacccggcc cggcgcctcg ctgtgggcgc gcttctacga cctggatgga
900
cagcagcctc tgttcgtcga ccgcgacagc aagcccgtcc cgttcgccag cctgcccaac
960
gagcgccgca ccggctatgc ctggtacggc acctggccgg agaagctgct ggcgcaggaa
1020
ctcccgcgct ggcgcgaggt ccatgccgcc ggcgccgcgc cctga
1065

<210> 82
<211> 354
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(30)

<221> DOMAIN
<222> (31)...(354)
<223> Catalytic domain

<400> 82
Met Thr Leu Pro Val Val Ser Leu Arg Val Leu Leu Ala Leu Leu Ala
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Thr Leu Pro Val Ala Cys Ala Gly Ala Ala Val Ser Ala Ala Ala Thr
            20   25   30
Asp Pro Val Ala Glu Asn Met Leu Leu Leu Gln Thr Ala Ser Gly Gly
        35   40   45
Trp Ser Lys His Tyr Arg Gly Lys Lys Val Asp Tyr Thr Arg Asn Tyr
    50   55   60
Asp Thr Ala Glu Arg Ala Ala Leu Arg Ala Pro Gly Arg His Asp Asp
65   70   75   80
Ala Thr Ile Asp Asn Lys Ala Thr Thr Ser Glu Ile Ala Tyr Leu Val
                85   90   95
Gln Ala His Ala Arg Thr Gly Asn Pro Ala Tyr Leu Asp Gly Ala Arg
            100   105   110
Arg Gly Val Glu Tyr Leu Leu Arg Ala Gln Tyr Pro Asn Gly Gly Trp
        115   120   125
Pro Gln Phe Tyr Pro Asp His Ser Ser Tyr Arg His Gln Ile Thr Leu
    130   135   140
Asn Asp Asp Ala Met Val His Ala Ile Thr Val Leu Gln Asp Ile Ala
145   150   155   160
Ala Gly Arg Asp Gly Met Gln Ala Leu Thr Pro Glu Phe Gly Val Arg
                165   170   175
Ala Ala Ala Ala Ala Gln Arg Gly Ile Gly Asn Leu Leu Glu Leu Gln
            180   185   190
Val Arg Ile Asp Gly Glu Pro Thr Ile Trp Ala Ala Gln Tyr Asp Glu
        195   200   205
His Ser Leu Gln Pro Ala Lys Ala Arg Ala Tyr Glu Leu Pro Ser Leu

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    210                 215                 220
Ala Val Ala Glu Ser Val Gly Val Val Arg Leu Leu Met Arg Gln Pro
225                 230                 235                 240
Arg Pro Asp Ala Arg Thr Val Ala Ala Ile Glu Ser Ala Ala Arg Trp
                245                 250                 255
Leu Glu Ala His Arg Leu His Asp Leu Ala Leu Glu Arg Val Asp Ala
            260                 265                 270
Pro Ala Glu Glu Thr Gly Lys Asp Val Arg Val Val Thr Arg Pro Gly
        275                 280                 285
Ala Ser Leu Trp Ala Arg Phe Tyr Asp Leu Asp Gly Gln Gln Pro Leu
    290                 295                 300
Phe Val Asp Arg Asp Ser Lys Pro Val Pro Phe Ala Ser Leu Pro Asn
305                 310                 315                 320
Glu Arg Arg Thr Gly Tyr Ala Trp Tyr Gly Thr Trp Pro Glu Lys Leu
                325                 330                 335
Leu Ala Gln Glu Leu Pro Arg Trp Arg Glu Val His Ala Ala Gly Ala
            340                 345                 350
Ala Pro
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<210> 83
<211> 3618
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 83
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120
gaaaaaatgg cagaaaccga cttccgggat acagggttag agaatggcca gaagtattac
180
tatgttgtat ctgccgaaac gagtagcggt gagagtgcag attcacaagc tataacggct
240
gtgcctgtag cgccattgca agctccgacc ggcctttcag caagtcatgg caatggcggg
300
gtaaccattc attgggaatc cgtcaatggt gccgagtctt accaagtctt gcgcagtaaa
360
caaaagggca tcggctatga agtcatcaaa aacggtgtaa cggaaaccag ttatacagat
420
accgggattc ccgatggcga gaagtactat tatgtcgtat ccgccaagaa cgatacagct
480
gaaagtgcaa attcccaacc gattaacggt gctgctgtat cgacgagtgg tgtaccagcc
540
attccaaacg gtatgaacgc tactgccggt gatggcagag ctgccttaac ctggtccgct
600
gtatccggcg cagattccta tagcatcaag cgcggtgagt ttaacagtgg tcaatatgag
660
gtcattgcta aaaatataca ctctaccggt tatcaagata taggccttac aaacggtgat
720
acctatgatt atgtgatttc cgctgtcaat gagcaagggg aaagtttagg ctccgaaccc
780
atcgccgtta ctcctgcgaa agtaacggtt gtagcgaaag aaggcggaga ctttaaaacg
840
attcaagaag ccattgatgc tgcacctgat aacagtacga aacggcatgt tatttttata
900
aaaaatggtc aatatcgtga aaagcttacg atccctaaga gcaaaaccaa tctgagtttt
960
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gtaggggaaa gtaaggaagg gaccgtgctt gtttttaatg ataatgcaaa tacgcctggg
1020
ccagacggca aaccattagg cacttccaat agttcaagta tctttatcta tgccaatgat
1080
tttattgccc aaaatttaac catccagaac gactctggtc aaggaacagg tcaagcagtt
1140
gccgcttatg taagggccga tcgtctctac tttgaaaacg tgcagttttt aggataccag
1200
gatacattat atgcccatac gggaagacag tattataaaa actgctacgt agaaggggat
1260
gtggatttca tttttggcgg agccacagcc ttgtttgata cctgtcacct tcatagcaag
1320
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1380
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1440
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1500
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1560
aataacatgg ggccaggggc agacccgaaa aagcgggatc catggaccac acaattaacg
1620
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1680
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1740
caacgagatt ccattgtcaa tacaccaagc tttacaatta caggtcaagt ggataaagaa
1800
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1860
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1920
aatcaggcta ttcctgcagt gttaaaaatt gtttatgatc atgagaaacc tgtcgtatcc
1980
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2040
ccgattacag ggaagctgaa cgaagcagga acagttatgg tgaatggtga gaaagtaaat
2100
gtatcggaaa agttgacgtt tagtacaaaa gtcattttaa agccggggtt aaataacatt
2160
acgattaccg ctgttgatca ggcagggaat gaagccgaat ctatcactat caatgtggtt
2220
ccaaaaggga atgctgttcc agacggtccc gtcaagatta tcaaaagtga aacaacaaat
2280
gcaaataccg ttgaggttac ttttaatagc aagctagaaa aatttgattc tagtgatatt
2340
gcattgcaaa cggctacgaa cgtttgggca gctctcaatc ctggtttgaa acaattgatg
2400
acagtggaaa gcattaccac aaaagtgaat aaggataacc aaaccgtagc ggtgatcaaa
2460
acgaaggaag cctttcaaga agatggaacc attacgctcc caaaagttga agatccgttt
2520
catattcaat atttgaatgc cgattattat accggggatc gtacgcagga cattaagcat
2580
gcggatgccc tcttaacctg gcagatggat catggcggct ggtttaaaaa ctgggtggaa
2640
aaatataaac ggccatggga tgggaaagaa ccaaaatctg aatggtattc gactaatcat
2700
ggtgaactag ggacgattga taatgacgca acaacaaacg agattctctt tttagctctg
2760
atgtataaag aaacaggtga tgctcgttat aaggattccg ttttaaaagg aattgatttt

2820
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2880
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2940
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3000
cagattgatg atgcattggg ccgtgggctg gattatatgt taaaatcgca aattaaggta
3060
gacggtgaag taaccgcatg gtgtgctcag catgaccctg tgacgtatga accgaaaggg
3120
gctcgtgcgt atgaacatcc ttcaatctct ggttcggaat ctgtagggat tgtccagtat
3180
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3240
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3300
tatttctacc cggacgccaa cagcaatacg tggtaccgct tctatgaaat tggcaccaat
3360
cgcccgattt tctcaggaag agacggtgtc attaaacaca acatcttaga gattgaaaaa
3420
gaaagaagag acggctaccg ctgggcagga gaatggccgc aaaaattatt aaatatcgcc
3480
aacacaactg gctactacga aaacagagta tacgtagaag tcgttgggga tcagtctaaa
3540
aacgccgctg gcgaatcttt ggaaatagga aacttatata gaatagaggc ctcggcttcc
3600
ggttctacaa gcaagtaa
3618

<210> 84
<211> 1205
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (268)...(556)
<223> Pectin methyl esterase domain

<221> DOMAIN
<222> (782)...(1164)
<223> Catalytic domain

<400> 84
Met Thr Ala Leu Ser Arg Asn Ser Gln Val Asp Val Ser Trp Glu Pro
 1   5   10   15
Ser Ser Ala Gln Gln Val Thr Tyr Asn Leu Lys Arg Ser Thr Thr Lys
            20   25   30
Glu Gly Pro Tyr Gln Thr Ile Ala Glu Lys Met Ala Glu Thr Asp Phe
        35   40   45
Arg Asp Thr Gly Leu Glu Asn Gly Gln Lys Tyr Tyr Tyr Val Val Ser
    50   55   60
Ala Glu Thr Ser Ser Gly Glu Ser Ala Asp Ser Gln Ala Ile Thr Ala
65   70   75   80
Val Pro Val Ala Pro Leu Gln Ala Pro Thr Gly Leu Ser Ala Ser His
                85   90   95
Gly Asn Gly Gly Val Thr Ile His Trp Glu Ser Val Asn Gly Ala Glu
            100   105   110

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Ser Tyr Gln Val Leu Arg Ser Lys Gln Lys Gly Ile Gly Tyr Glu Val
        115                 120                 125
Ile Lys Asn Gly Val Thr Glu Thr Ser Tyr Thr Asp Thr Gly Ile Pro
    130                 135                 140
Asp Gly Glu Lys Tyr Tyr Tyr Val Val Ser Ala Lys Asn Asp Thr Ala
145                 150                 155                 160
Glu Ser Ala Asn Ser Gln Pro Ile Asn Gly Ala Ala Val Ser Thr Ser
                165                 170                 175
Gly Val Pro Ala Ile Pro Asn Gly Met Asn Ala Thr Ala Gly Asp Gly
            180                 185                 190
Arg Ala Ala Leu Thr Trp Ser Ala Val Ser Gly Ala Asp Ser Tyr Ser
        195                 200                 205
Ile Lys Arg Gly Glu Phe Asn Ser Gly Gln Tyr Glu Val Ile Ala Lys
    210                 215                 220
Asn Ile His Ser Thr Gly Tyr Gln Asp Ile Gly Leu Thr Asn Gly Asp
225                 230                 235                 240
Thr Tyr Asp Tyr Val Ile Ser Ala Val Asn Glu Gln Gly Glu Ser Leu
                245                 250                 255
Gly Ser Glu Pro Ile Ala Val Thr Pro Ala Lys Val Thr Val Val Ala
            260                 265                 270
Lys Glu Gly Gly Asp Phe Lys Thr Ile Gln Glu Ala Ile Asp Ala Ala
        275                 280                 285
Pro Asp Asn Ser Thr Lys Arg His Val Ile Phe Ile Lys Asn Gly Gln
    290                 295                 300
Tyr Arg Glu Lys Leu Thr Ile Pro Lys Ser Lys Thr Asn Leu Ser Phe
305                 310                 315                 320
Val Gly Glu Ser Lys Glu Gly Thr Val Leu Val Phe Asn Asp Asn Ala
                325                 330                 335
Asn Thr Pro Gly Pro Asp Gly Lys Pro Leu Gly Thr Ser Asn Ser Ser
            340                 345                 350
Ser Ile Phe Ile Tyr Ala Asn Asp Phe Ile Ala Gln Asn Leu Thr Ile
        355                 360                 365
Gln Asn Asp Ser Gly Gln Gly Thr Gly Gln Ala Val Ala Ala Tyr Val
    370                 375                 380
Arg Ala Asp Arg Leu Tyr Phe Glu Asn Val Gln Phe Leu Gly Tyr Gln
385                 390                 395                 400
Asp Thr Leu Tyr Ala His Thr Gly Arg Gln Tyr Tyr Lys Asn Cys Tyr
                405                 410                 415
Val Glu Gly Asp Val Asp Phe Ile Phe Gly Gly Ala Thr Ala Leu Phe
            420                 425                 430
Asp Thr Cys His Leu His Ser Lys Arg Thr Gly Ser Lys Leu Thr Ala
        435                 440                 445
Ala Ser Thr Asp Gln Val Thr Pro Tyr Gly Tyr Val Phe Leu Asp Ser
    450                 455                 460
Lys Ile Thr Ser Asp Glu Gly Val Thr Asn Val His Leu Gly Arg Pro
465                 470                 475                 480
Trp Arg Pro Tyr Ser Ala Val Thr Tyr Ile Asn Thr Glu Met Asp Ala
                485                 490                 495
Ser Ile Val Pro Asp Gly Trp Asp Asn Trp Gly Lys Val Glu Asn Glu
            500                 505                 510
Lys Thr Ala Arg Tyr Ser Glu Tyr Asn Asn Met Gly Pro Gly Ala Asp
        515                 520                 525
Pro Lys Lys Arg Asp Pro Trp Thr Thr Gln Leu Thr Pro Glu Glu Ala
    530                 535                 540
Asn Gln Tyr Thr Val Gln Asn Val Met Lys Gly Ser Asp Gly Trp Asp
545                 550                 555                 560
Pro Glu Arg Ile Gly Ile Ile Pro Leu Ser Pro Leu Ser Ala Pro Ile
                565                 570                 575
Ile Ser Leu Asp Gln Arg Asp Ser Ile Val Asn Thr Pro Ser Phe Thr
            580                 585                 590
Ile Thr Gly Gln Val Asp Lys Glu Ala Ala Val Ser Val Asn Gly Lys
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595 600 605

Glu Ile Ser Leu Gln Lys Asp Gly Ser Phe Ser Thr Thr Val Val Leu
610 615 620

Asn Asp Gly Leu Asn Thr Ile Thr Val Gly Ala Val Asp Ala Ala Gly
625 630 635 640

Asn Gln Ala Ile Pro Ala Val Leu Lys Ile Val Tyr Asp His Glu Lys
645 650 655

Pro Val Val Ser Ile Asp Asp Leu Lys Gly Glu Lys Asn Gly Asn His
660 665 670

Tyr Asn Val Ile Tyr Asn Pro Leu Pro Ile Thr Gly Lys Leu Asn Glu
675 680 685

Ala Gly Thr Val Met Val Asn Gly Glu Lys Val Asn Val Ser Glu Lys
690 695 700

Leu Thr Phe Ser Thr Lys Val Ile Leu Lys Pro Gly Leu Asn Asn Ile
705 710 715 720

Thr Ile Thr Ala Val Asp Gln Ala Gly Asn Glu Ala Glu Ser Ile Thr
725 730 735

Ile Asn Val Val Pro Lys Gly Asn Ala Val Pro Asp Gly Pro Val Lys
740 745 750

Ile Ile Lys Ser Glu Thr Thr Asn Ala Asn Thr Val Glu Val Thr Phe
755 760 765

Asn Ser Lys Leu Glu Lys Phe Asp Ser Ser Asp Ile Ala Leu Gln Thr
770 775 780

Ala Thr Asn Val Trp Ala Ala Leu Asn Pro Gly Leu Lys Gln Leu Met
785 790 795 800

Thr Val Glu Ser Ile Thr Thr Lys Val Asn Lys Asp Asn Gln Thr Val
805 810 815

Ala Val Ile Lys Thr Lys Glu Ala Phe Gln Glu Asp Gly Thr Ile Thr
820 825 830

Leu Pro Lys Val Glu Asp Pro Phe His Ile Gln Tyr Leu Asn Ala Asp
835 840 845

Tyr Tyr Thr Gly Asp Arg Thr Gln Asp Ile Lys His Ala Asp Ala Leu
850 855 860

Leu Thr Trp Gln Met Asp His Gly Gly Trp Phe Lys Asn Trp Val Glu
865 870 875 880

Lys Tyr Lys Arg Pro Trp Asp Gly Lys Glu Pro Lys Ser Glu Trp Tyr
885 890 895

Ser Thr Asn His Gly Glu Leu Gly Thr Ile Asp Asn Asp Ala Thr Thr
900 905 910

Asn Glu Ile Leu Phe Leu Ala Leu Met Tyr Lys Glu Thr Gly Asp Ala
915 920 925

Arg Tyr Lys Asp Ser Val Leu Lys Gly Ile Asp Phe Leu Leu Glu Met
930 935 940

Gln Val Asp Ser Gly Gly Trp Pro Gln Val Tyr Pro Ala Arg Ser Gly
945 950 955 960

Tyr Ser Asp Tyr Val Thr Phe Asn Asp Asn Ala Met Val Arg Val Met
965 970 975

Ser Val Leu Thr Met Val Lys Glu Lys Lys Tyr Pro Phe Asn Ser Asn
980 985 990

Leu Gly Asp Glu Gln Leu Ser Glu Gln Ile Asp Asp Ala Leu Gly Arg
995 1000 1005

Gly Leu Asp Tyr Met Leu Lys Ser Gln Ile Lys Val Asp Gly Glu Val
1010 1015 1020

Thr Ala Trp Cys Ala Gln His Asp Pro Val Thr Tyr Glu Pro Lys Gly
1025 1030 1035 1040

Ala Arg Ala Tyr Glu His Pro Ser Ile Ser Gly Ser Glu Ser Val Gly
1045 1050 1055

Ile Val Gln Tyr Leu Met Ser Leu Pro Asn Pro Ser Thr Glu Val Gln
1060 1065 1070

Ala Ala Ile His Gly Ala Leu Asn Trp Phe Glu Glu Ala Lys Leu Ala
1075 1080 1085

Gly Thr Lys Tyr Val Ser Gly Asp Pro Asn Gly Gln Tyr Phe Tyr Pro
1090 1095 1100
Asp Ala Asn Ser Asn Thr Trp Tyr Arg Phe Tyr Glu Ile Gly Thr Asn
1105 1110 1115 1120
Arg Pro Ile Phe Ser Gly Arg Asp Gly Val Ile Lys His Asn Ile Leu
1125 1130 1135
Glu Ile Glu Lys Glu Arg Arg Asp Gly Tyr Arg Trp Ala Gly Glu Trp
1140 1145 1150
Pro Gln Lys Leu Leu Asn Ile Ala Asn Thr Thr Gly Tyr Tyr Glu Asn
1155 1160 1165
Arg Val Tyr Val Glu Val Val Gly Asp Gln Ser Lys Asn Ala Ala Gly
1170 1175 1180
Glu Ser Leu Glu Ile Gly Asn Leu Tyr Arg Ile Glu Ala Ser Ala Ser
1185 1190 1195 1200
Gly Ser Thr Ser Lys
1205

<210> 85
<211> 1152
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 85
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ggtgttgagg caaagctgtt tcagcgcgag cggttcttca gcctcgctgc ggagcacact
120
tctaagaaaa atgatcagga agtcggcgcg atcgcgtgga aagatgcaca tggaaagccg
180
gatgagtggt atgcgagtgt tgaggcactg cggatggccg ataacgtcgt tctctatcaa
240
cgcgactcag gtggttggcc caagaacatc gacatggcga aggcactcaa cgatcgtgag
300
caggctgcga tcctccgcca gaagaaaaag aacgactcca cgatcgacaa tggtgcgact
360
cacacacagt tatcctttct ggcgcgcgtc tatacagcac agcgtcagga gcgacatcgc
420
gagtcgtttt tcaaaggatt ggattactta ctgaatgcgc agtatccaaa tggaggctgg
480
ccgcagtttt atccgaaccc gacgggctat cacaagcaca ttacttacaa cgacggtgcg
540
atgattggtg tgatgaaggt gctgcgcgat atcgctgcgg cgaagccttt gtacgctttt
600
gtcgacgaag ctcggcgcgc gaaggcgacg agtgcagttg aaaaagggat cgagtgcatt
660
ttgaaaacgc aggtggtggt agatgggcgt cgcactgtgt ggagtgcgca acatgatgaa
720
gtaacgttag cgccagctcc tgcgcgaacc ttcgagttaa cttcgttgag cggcggtgag
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960
agctcggttt gggcgcgctt ttatgagatt ggcacgaacc ggccgatctt ttccgggcgc
1020
gatggagtgg tcaaatacga cgtggcgcag atcgaacacg agcggcggac gaattatgag

1080
tggtacgttg atgaagcagc caagctgctg aagaaagagt atccggcctg gcggaaaaga
1140
acatctctgt ga
1152

<210> 86
<211> 383
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(383)
<223> Catalytic domain

<400> 86
Met Ser Val Gly Pro Gly Ala Asn Pro Lys Ala Arg Val Pro Trp Ser
 1   5   10   15
Lys Gln Leu Ser Gly Val Glu Ala Lys Leu Phe Gln Arg Glu Arg Phe
            20   25   30
Phe Ser Leu Ala Ala Glu His Thr Ser Lys Lys Asn Asp Gln Glu Val
        35   40   45
Gly Ala Ile Ala Trp Lys Asp Ala His Gly Lys Pro Asp Glu Trp Tyr
    50   55   60
Ala Ser Val Glu Ala Leu Arg Met Ala Asp Asn Val Val Leu Tyr Gln
65   70   75   80
Arg Asp Ser Gly Gly Trp Pro Lys Asn Ile Asp Met Ala Lys Ala Leu
                85   90   95
Asn Asp Arg Glu Gln Ala Ala Ile Leu Arg Gln Lys Lys Lys Asn Asp
            100   105   110
Ser Thr Ile Asp Asn Gly Ala Thr His Thr Gln Leu Ser Phe Leu Ala
        115   120   125
Arg Val Tyr Thr Ala Gln Arg Gln Glu Arg His Arg Glu Ser Phe Phe
    130   135   140
Lys Gly Leu Asp Tyr Leu Leu Asn Ala Gln Tyr Pro Asn Gly Gly Trp
145   150   155   160
Pro Gln Phe Tyr Pro Asn Pro Thr Gly Tyr His Lys His Ile Thr Tyr
                165   170   175
Asn Asp Gly Ala Met Ile Gly Val Met Lys Val Leu Arg Asp Ile Ala
            180   185   190
Ala Ala Lys Pro Leu Tyr Ala Phe Val Asp Glu Ala Arg Arg Ala Lys
        195   200   205
Ala Thr Ser Ala Val Glu Lys Gly Ile Glu Cys Ile Leu Lys Thr Gln
    210   215   220
Val Val Val Asp Gly Arg Arg Thr Val Trp Ser Ala Gln His Asp Glu
225   230   235   240
Val Thr Leu Ala Pro Ala Pro Ala Arg Thr Phe Glu Leu Thr Ser Leu
                245   250   255
Ser Gly Gly Glu Ser Val Asp Ile Val Arg Phe Leu Met Ser Ile Lys
            260   265   270
Asp Pro Ser Pro Lys Val Val Asp Ala Val Glu Ser Ala Val Lys Trp
        275   280   285
Phe Glu Gln Ser Glu Leu Lys Gly Val Lys Trp Val Lys Lys Ala Asp
    290   295   300
Ala Ser Lys Pro Gly Gly Phe Asp Cys Val Val Val Lys Asp Pro Glu
305   310   315   320
Ser Ser Val Trp Ala Arg Phe Tyr Glu Ile Gly Thr Asn Arg Pro Ile
                325   330   335

Phe Ser Gly Arg Asp Gly Val Val Lys Tyr Asp Val Ala Gln Ile Glu
340 345 350
His Glu Arg Arg Thr Asn Tyr Glu Trp Tyr Val Asp Glu Ala Ala Lys
355 360 365
Leu Leu Lys Lys Glu Tyr Pro Ala Trp Arg Lys Arg Thr Ser Leu
370 375 380

<210> 87
<211> 1698
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 87
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gcagtggcga tgtttgcagg ttcttcagta ttcgcagcgg ctacaggtgg tttttccacg
120
actgatggcg gtgcggcaag cggctcgcaa tccttcacgg cggccaacct tgaccagctc
180
aacaccattg ttgccaatgc gaagagtggc ggttacccgg ttgtgattac ctataccggt
240
aatgaagaca gcttgattaa ccagatgatc aaagaccaca ccgtggattc ttcaggcaac
300
tgcccgaacc cacgctggag tgaaacctac cgcaaggtag aaattaagga gatgaccaaa
360
ggtgtcacca tcatcggtgc caatggttct tcggcaaact tcggtattgt ggtgaacaag
420
tccagcaatg tgattatccg caacatgaaa atcggtgcgc tggccggtgc cagcaacgac
480
gcggatatga ttcgtatcga tagcggcact aacgtatggg ttgaccacaa cgaattgttc
540
gcggtgaaca acgaatgtaa aggttcaccg gatggcgatt tgaccttcga aagcgccatc
600
gacatcaaga aagattcaca caacatcacc gtgtcttaca acctgattcg cgacagcaaa
660
aaagtgggcc ttgatggttc cagcagcagc gatatcgccg gtggccgcga gatcactttc
720
caccacaaca tttacaaaaa cgtgaatgca cgcttgccgt tgcaacgcgg tggctggacg
780
cacatgtata acaacctgta cgacggcatt accggttccg gtatcaacgt acgtcaggcc
840
ggttatgcgt tgattgaaag caactggttc caaaatgcgg ttaacccggt gacttgccgt
900
tacgacagca gcaactgcgg tttctgggat ctgcgcaata acaacgtgaa gtcgccagca
960
gatttcgcga cctataacat cacctggacc agcggcggca ctattgatgc aaccaactgg
1020
acgaccaccg ctccgttccc gatcagcatt ccttacagct actcgccggt gtctccacag
1080
tgcgtgaagg acaagttggc cagcgttgcg ggtgtgggta aaaacggtgc agttctgaac
1140
tcatcagtgt gtggtggaag cagctctgtt ccatcatcaa gctcagtcgc tactacttcc
1200
aaatcatcca gctcggtagc aaccagcaag tccagctccg tcgctacgac gtccagtaag
1260
tcatccagct cggtagtgcc atcatcatca agctcaagtt cagtggttaa taacggcagc
1320
atcgcgttaa ccgccactgc taccggcaat agcattgtcc tgagctggtc gccgaacaac

1380
ctgacactgg gcacccagga ggtgtatcgc gataccgatt cagacccaag tggccgtgtg
1440
cgtattgctg ccctgagttc cagcactcgc atgtacaccg atgccactgc atcggcgggc
1500
caaacgttct actactggat caaaaacacc accaacggtg taaccaccaa ttccaatgcg
1560
gcttcggcgg caattggcga tgcagctcgc gccattcgcg catgcgcagg aaaccgagga
1620
agtggcgctc gcaccagtcg cgcagtttcg actgggtcaa atcctcgtgg gcctgccggt
1680
agccatccca gagcttga
1698

<210> 88
<211> 565
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(32)

<221> DOMAIN
<222> (33)...(375)
<223> Catalytic domain

<400> 88
Met Ser Thr Thr Lys Cys Phe Asn Thr Ala Pro Gly Phe Thr Leu Lys
 1   5   10   15
Ala Val Ala Ala Ala Val Ala Met Phe Ala Gly Ser Ser Val Phe Ala
            20   25   30
Ala Ala Thr Gly Gly Phe Ser Thr Thr Asp Gly Gly Ala Ala Ser Gly
        35   40   45
Ser Gln Ser Phe Thr Ala Ala Asn Leu Asp Gln Leu Asn Thr Ile Val
    50   55   60
Ala Asn Ala Lys Ser Gly Gly Tyr Pro Val Val Ile Thr Tyr Thr Gly
65   70   75   80
Asn Glu Asp Ser Leu Ile Asn Gln Met Ile Lys Asp His Thr Val Asp
                85   90   95
Ser Ser Gly Asn Cys Pro Asn Pro Arg Trp Ser Glu Thr Tyr Arg Lys
            100   105   110
Val Glu Ile Lys Glu Met Thr Lys Gly Val Thr Ile Ile Gly Ala Asn
        115   120   125
Gly Ser Ser Ala Asn Phe Gly Ile Val Val Asn Lys Ser Ser Asn Val
    130   135   140
Ile Ile Arg Asn Met Lys Ile Gly Ala Leu Ala Gly Ala Ser Asn Asp
145   150   155   160
Ala Asp Met Ile Arg Ile Asp Ser Gly Thr Asn Val Trp Val Asp His
                165   170   175
Asn Glu Leu Phe Ala Val Asn Asn Glu Cys Lys Gly Ser Pro Asp Gly
            180   185   190
Asp Leu Thr Phe Glu Ser Ala Ile Asp Ile Lys Lys Asp Ser His Asn
        195   200   205
Ile Thr Val Ser Tyr Asn Leu Ile Arg Asp Ser Lys Lys Val Gly Leu
    210   215   220
Asp Gly Ser Ser Ser Ser Asp Ile Ala Gly Gly Arg Glu Ile Thr Phe
225   230   235   240
His His Asn Ile Tyr Lys Asn Val Asn Ala Arg Leu Pro Leu Gln Arg

245 250 255
Gly Gly Trp Thr His Met Tyr Asn Asn Leu Tyr Asp Gly Ile Thr Gly
260 265 270
Ser Gly Ile Asn Val Arg Gln Ala Gly Tyr Ala Leu Ile Glu Ser Asn
275 280 285
Trp Phe Gln Asn Ala Val Asn Pro Val Thr Cys Arg Tyr Asp Ser Ser
290 295 300
Asn Cys Gly Phe Trp Asp Leu Arg Asn Asn Asn Val Lys Ser Pro Ala
305 310 315 320
Asp Phe Ala Thr Tyr Asn Ile Thr Trp Thr Ser Gly Gly Thr Ile Asp
325 330 335
Ala Thr Asn Trp Thr Thr Thr Ala Pro Phe Pro Ile Ser Ile Pro Tyr
340 345 350
Ser Tyr Ser Pro Val Ser Pro Gln Cys Val Lys Asp Lys Leu Ala Ser
355 360 365
Val Ala Gly Val Gly Lys Asn Gly Ala Val Leu Asn Ser Ser Val Cys
370 375 380
Gly Gly Ser Ser Ser Val Pro Ser Ser Ser Ser Val Ala Thr Thr Ser
385 390 395 400
Lys Ser Ser Ser Ser Val Ala Thr Ser Lys Ser Ser Ser Val Ala Thr
405 410 415
Thr Ser Ser Lys Ser Ser Ser Ser Val Val Pro Ser Ser Ser Ser Ser
420 425 430
Ser Ser Val Val Asn Asn Gly Ser Ile Ala Leu Thr Ala Thr Ala Thr
435 440 445
Gly Asn Ser Ile Val Leu Ser Trp Ser Pro Asn Asn Leu Thr Leu Gly
450 455 460
Thr Gln Glu Val Tyr Arg Asp Thr Asp Ser Asp Pro Ser Gly Arg Val
465 470 475 480
Arg Ile Ala Ala Leu Ser Ser Ser Thr Arg Met Tyr Thr Asp Ala Thr
485 490 495
Ala Ser Ala Gly Gln Thr Phe Tyr Tyr Trp Ile Lys Asn Thr Thr Asn
500 505 510
Gly Val Thr Thr Asn Ser Asn Ala Ala Ser Ala Ala Ile Gly Asp Ala
515 520 525
Ala Arg Ala Ile Arg Ala Cys Ala Gly Asn Arg Gly Ser Gly Ala Arg
530 535 540
Thr Ser Arg Ala Val Ser Thr Gly Ser Asn Pro Arg Gly Pro Ala Gly
545 550 555 560
Ser His Pro Arg Ala
565

<210> 89
<211> 1377
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 89
atgacgacgc gacgcgaatt cattcgagat cttttggttg gcggcgtagt ggtcgctgtt
60
gcaccgcgtt tcctggcgtt ttcttcggtg gcgagtccgt gggaaacggt gatgccttcg
120
atcctcgaac gcatcaagcc accgcgtttt ccgaaacgca cgtgctatct caaccggttt
180
ggagcaaaag gcgacgggca aactgattgc acttcagctt ttcgacgcgc aatcgatcag
240
tgttcgaaag cgggcggtgg caaagtgatc gttccgcagg gaatgtatct caccggcgca
300

attcacttga agagcaacgt caatctcgag atctccgaag gcgcgacgat caagttcagt
360
caaaacccga aagactatct cccggtggtt ttttcgcgtt gggaaggcgt cgaagtattc
420
aactactcac ctttcatcta cgcatttgaa cagcagaaca tcgcgatcac gggcaagggc
480
acgctcgatg ggcagagtga taacgaacac tggtggccat ggaacggacg cgccaggtac
540
ggttggaaag aagggatgag ccaccagcgt ccggatcgaa acgcgctctt tgcgatggcg
600
gaaaaaggtg tttcggttcg cgaacgtgtt ttcggcgagg gtcattactt aaggccgcag
660
ttcattcagc cgtatcgctg ccagaacgta ttgatcgacg gagttacgat acgaaactcg
720
ccgatgtggg aaattcatcc ggtgctgtgc cggaatgtca tcgtgcaaaa cgtgcacatt
780
aacagtcatg gaccaaacaa cgatggctgc aatcccgagt cgtgcactga tgtgctgatt
840
aagaactgtt acttcgacac tggcgacgac tgtatcgcgg tcaaatcagg acgcaacgcg
900
gacggccggc ggcttaaagc gccgacagag aacgtgatcg tgcaagactg tcaaatgaaa
960
gatggacacg gcgggatcac tgtcggcagt gagatctcag gcggtgtgag aaatctgttt
1020
gcggagaact gccggcttga tagtccaaac ctggaccatg ctttgcgggt taagaacaac
1080
gcgatgcgtg gagggctgct cgagaatttg cacttccgaa acatcgaagt tggtcaggtg
1140
gcgcatgcag tgatcacgat cgattttaat tacgaggaag gcgcgaaagg atcgttcacg
1200
ccggtggttc gtgactacac tgtcgatggt ttgcgcagca cgcgaagcaa atacgcgctc
1260
gacgttcaag gtctgtcggg cgcgccgatc gtaaatctgc gtctgacgaa ttgcacgttc
1320
gacaatgttg ccgaagggaa cgtcgtgaag aatgttaagg acgcgacaat tcaaaaa
1377

<210> 90
<211> 459
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(31)

<221> DOMAIN
<222> (32)...(459)
<223> Catalytic domain

<400> 90
Met Thr Thr Arg Arg Glu Phe Ile Arg Asp Leu Leu Val Gly Gly Val
 1   5   10   15
Val Val Ala Val Ala Pro Arg Phe Leu Ala Phe Ser Ser Val Ala Ser
            20   25   30
Pro Trp Glu Thr Val Met Pro Ser Ile Leu Glu Arg Ile Lys Pro Pro
        35   40   45
Arg Phe Pro Lys Arg Thr Cys Tyr Leu Asn Arg Phe Gly Ala Lys Gly
    50   55   60

```
Asp Gly Gln Thr Asp Cys Thr Ser Ala Phe Arg Arg Ala Ile Asp Gln
65                  70                  75                  80
Cys Ser Lys Ala Gly Gly Gly Lys Val Ile Val Pro Gln Gly Met Tyr
                85                  90                  95
Leu Thr Gly Ala Ile His Leu Lys Ser Asn Val Asn Leu Glu Ile Ser
            100                 105                 110
Glu Gly Ala Thr Ile Lys Phe Ser Gln Asn Pro Lys Asp Tyr Leu Pro
        115                 120                 125
Val Val Phe Ser Arg Trp Glu Gly Val Glu Val Phe Asn Tyr Ser Pro
    130                 135                 140
Phe Ile Tyr Ala Phe Glu Gln Gln Asn Ile Ala Ile Thr Gly Lys Gly
145                 150                 155                 160
Thr Leu Asp Gly Gln Ser Asp Asn Glu His Trp Trp Pro Trp Asn Gly
                165                 170                 175
Arg Ala Arg Tyr Gly Trp Lys Glu Gly Met Ser His Gln Arg Pro Asp
            180                 185                 190
Arg Asn Ala Leu Phe Ala Met Ala Glu Lys Gly Val Ser Val Arg Glu
        195                 200                 205
Arg Val Phe Gly Glu Gly His Tyr Leu Arg Pro Gln Phe Ile Gln Pro
    210                 215                 220
Tyr Arg Cys Gln Asn Val Leu Ile Asp Gly Val Thr Ile Arg Asn Ser
225                 230                 235                 240
Pro Met Trp Glu Ile His Pro Val Leu Cys Arg Asn Val Ile Val Gln
                245                 250                 255
Asn Val His Ile Asn Ser His Gly Pro Asn Asn Asp Gly Cys Asn Pro
            260                 265                 270
Glu Ser Cys Thr Asp Val Leu Ile Lys Asn Cys Tyr Phe Asp Thr Gly
        275                 280                 285
Asp Asp Cys Ile Ala Val Lys Ser Gly Arg Asn Ala Asp Gly Arg Arg
    290                 295                 300
Leu Lys Ala Pro Thr Glu Asn Val Ile Val Gln Asp Cys Gln Met Lys
305                 310                 315                 320
Asp Gly His Gly Gly Ile Thr Val Gly Ser Glu Ile Ser Gly Gly Val
                325                 330                 335
Arg Asn Leu Phe Ala Glu Asn Cys Arg Leu Asp Ser Pro Asn Leu Asp
            340                 345                 350
His Ala Leu Arg Val Lys Asn Asn Ala Met Arg Gly Gly Leu Leu Glu
        355                 360                 365
Asn Leu His Phe Arg Asn Ile Glu Val Gly Gln Val Ala His Ala Val
    370                 375                 380
Ile Thr Ile Asp Phe Asn Tyr Glu Glu Gly Ala Lys Gly Ser Phe Thr
385                 390                 395                 400
Pro Val Val Arg Asp Tyr Thr Val Asp Gly Leu Arg Ser Thr Arg Ser
                405                 410                 415
Lys Tyr Ala Leu Asp Val Gln Gly Leu Ser Gly Ala Pro Ile Val Asn
            420                 425                 430
Leu Arg Leu Thr Asn Cys Thr Phe Asp Asn Val Ala Glu Gly Asn Val
        435                 440                 445
Val Lys Asn Val Lys Asp Ala Thr Ile Gln Lys
    450                 455
```

<210> 91
<211> 1125
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 91
gtggtcctag gtaataacgg cggcagcttg agttgcgtcc aatatattgt gattgtgaaa

60
ggacccggtg gacctcgacc gccggtgaaa ccggccgtcc aggcgcccgt tagggttacc
120
tggagcgcat ccctagtcca gcggcccgaa tggtacggga gtgacgaagc gatccgcatc
180
gcggacaacg tcctcctcta ccagcgcaac accggcgggt ggccgaagga catagatatg
240
gccgagccca tcccggaaca caggaagtcc tttttcctca ccgagaagga gcggaccgat
300
gactcgacca tcgacaacgg tgccaccgtg acccagctca agtatctcgc ccgcgtctac
360
aaggcgacca ggctggaacg gttcaaggag ggcttcctca aaggtctcga ctacctcttg
420
gccgcccagt acccgaacgg cggctggccc cagtattatc ctaacttgag gggctactac
480
gccaacatca cttataacga caatgccatg gtgaacgtgc tcaccctcct ccagagcatc
540
gccaaaaagg ccccggagta cgacttcgtc gacccggcgc gccgggagaa ggccgcccgg
600
gccgtggcga aagggatcga ctgcatcctc aagacccaga tccgtgtcaa tggaaaactt
660
accgcctggt gcgcccagca tgacgccaag acgctggcgc ccgcgccggc ccgttcgtat
720
gagcttgagt ccatcagcgg tttcgagagc gtcgggatcg tccggttctt aatgagcctc
780
gagaatccga gcccgaaggt catcgaggcg gtagaggccg ccgtgaaatg gttcgaggag
840
gtcaagctta ccgggatcaa ggtggtcgag aaacccgacc cgtcccttcc gggcggttac
900
gaccgcgtgg tggtcgaaga ccccaacgcg ccgcccatct gggcccggtt ctacgagatc
960
ggcaccaacc gtcccttctt ctgcggccgc gatggtatca aaaaatacag cctggcggag
1020
atcgaacacg aacgccgggt cggttactcc tggtacacca atgccccggc ctacctcatc
1080
gagaaggagt atccgctctg gcgggccaaa caccctacca agtaa
1125

<210> 92
<211> 374
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(374)

<400> 92
Met Val Leu Gly Asn Asn Gly Gly Ser Leu Ser Cys Val Gln Tyr Ile
 1   5   10   15
Val Ile Val Lys Gly Pro Gly Gly Pro Arg Pro Pro Val Lys Pro Ala
            20   25   30
Val Gln Ala Pro Val Arg Val Thr Trp Ser Ala Ser Leu Val Gln Arg
        35   40   45
Pro Glu Trp Tyr Gly Ser Asp Glu Ala Ile Arg Ile Ala Asp Asn Val
    50   55   60
Leu Leu Tyr Gln Arg Asn Thr Gly Gly Trp Pro Lys Asp Ile Asp Met
65   70   75   80
Ala Glu Pro Ile Pro Glu His Arg Lys Ser Phe Phe Leu Thr Glu Lys

```
                85                  90                  95
Glu Arg Thr Asp Asp Ser Thr Ile Asp Asn Gly Ala Thr Val Thr Gln
            100                 105                 110
Leu Lys Tyr Leu Ala Arg Val Tyr Lys Ala Thr Arg Leu Glu Arg Phe
        115                 120                 125
Lys Glu Gly Phe Leu Lys Gly Leu Asp Tyr Leu Leu Ala Ala Gln Tyr
    130                 135                 140
Pro Asn Gly Gly Trp Pro Gln Tyr Tyr Pro Asn Leu Arg Gly Tyr Tyr
145                 150                 155                 160
Ala Asn Ile Thr Tyr Asn Asp Asn Ala Met Val Asn Val Leu Thr Leu
                165                 170                 175
Leu Gln Ser Ile Ala Lys Lys Ala Pro Glu Tyr Asp Phe Val Asp Pro
            180                 185                 190
Ala Arg Arg Glu Lys Ala Ala Arg Ala Val Ala Lys Gly Ile Asp Cys
        195                 200                 205
Ile Leu Lys Thr Gln Ile Arg Val Asn Gly Lys Leu Thr Ala Trp Cys
    210                 215                 220
Ala Gln His Asp Ala Lys Thr Leu Ala Pro Ala Pro Ala Arg Ser Tyr
225                 230                 235                 240
Glu Leu Glu Ser Ile Ser Gly Phe Glu Ser Val Gly Ile Val Arg Phe
                245                 250                 255
Leu Met Ser Leu Glu Asn Pro Ser Pro Lys Val Ile Glu Ala Val Glu
            260                 265                 270
Ala Ala Val Lys Trp Phe Glu Glu Val Lys Leu Thr Gly Ile Lys Val
        275                 280                 285
Val Glu Lys Pro Asp Pro Ser Leu Pro Gly Gly Tyr Asp Arg Val Val
    290                 295                 300
Val Glu Asp Pro Asn Ala Pro Pro Ile Trp Ala Arg Phe Tyr Glu Ile
305                 310                 315                 320
Gly Thr Asn Arg Pro Phe Phe Cys Gly Arg Asp Gly Ile Lys Lys Tyr
                325                 330                 335
Ser Leu Ala Glu Ile Glu His Glu Arg Arg Val Gly Tyr Ser Trp Tyr
            340                 345                 350
Thr Asn Ala Pro Ala Tyr Leu Ile Glu Lys Glu Tyr Pro Leu Trp Arg
        355                 360                 365
Ala Lys His Pro Thr Lys
    370
```

<210> 93
<211> 1062
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 93
gtggatccaa agaattggaa cccgaaaaaa gccgacgatt catggctcga aaagacgaaa
60
cccgattacc ggctggtctc ctggcgcgac gttttagatc aaactcagct ctggtacgcg
120
gtcgacgaag cgacgcgcat cgccaaccag gttttgctct ttcagcgcga taacggcggc
180
tgggaaaaaa acgtcgacat ggcggcgatg ctcactcaag ccgaacgaga aaaactcgtc
240
aaagaaaaat ctcacaccga tacgaccatc gacaacggcg cgacgaccac gcagctgcgt
300
tatctggcaa aagtcatcac ggcgaaaaac atcgaagctc ataaacagtc gtttctcaag
360
ggattggatt ttctgctcgc gatgcagtat gaaaacggag gatttccgca atattatcct
420

ttgaaaaacg attattcgcg cgagattact ttcaacgacg acgcgatgat caatgttctt
480
aaattgctgc gcgacgtggc aaaaaagaag gaagattatt tattcgtcga cgaagaccgg
540
cgcgccagag cggaaggcgc ggtcgaaaaa ggcgtccgcc tgatcttgaa aacacaggtc
600
gccatcgacg gcaaaaaaac gatctgggcg gcgcagtacg acgaaaacac tttgaaaccg
660
gcaaatgcga gaaagtttga gcccgcctcg ctcgcttcgc gcgaatcggt cagcgtggtc
720
agatttttga tgctcgacgc caaacccgac gaggaaaaaa tcggagcgat cgaatcggcg
780
atcgaatggt ttcaaaaaaa caaactgagc ggcattcgct gggaatcgaa aagcggagaa
840
aacctggtcg tcaaagacaa agcggcgccg ccgatctggg gaaggtttta tcaattcgaa
900
accatgcgcc ccatttttat cgggcgcgac gcggtgattc gctacgatgt catgcaaatc
960
gaagccgaac gccgcaacgg ctacggctgg tacacgaacg agccgaacga gcttttggac
1020
aaagattatc cgaaatggaa agagaaaatt aagaaaaatt ag
1062

<210> 94
<211> 353
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(353)

<400> 94
Met Asp Pro Lys Asn Trp Asn Pro Lys Lys Ala Asp Asp Ser Trp Leu
 1   5   10   15
Glu Lys Thr Lys Pro Asp Tyr Arg Leu Val Ser Trp Arg Asp Val Leu
            20   25   30
Asp Gln Thr Gln Leu Trp Tyr Ala Val Asp Glu Ala Thr Arg Ile Ala
        35   40   45
Asn Gln Val Leu Leu Phe Gln Arg Asp Asn Gly Gly Trp Glu Lys Asn
    50   55   60
Val Asp Met Ala Ala Met Leu Thr Gln Ala Glu Arg Glu Lys Leu Val
65   70   75   80
Lys Glu Lys Ser His Thr Asp Thr Thr Ile Asp Asn Gly Ala Thr Thr
                85   90   95
Thr Gln Leu Arg Tyr Leu Ala Lys Val Ile Thr Ala Lys Asn Ile Glu
            100   105   110
Ala His Lys Gln Ser Phe Leu Lys Gly Leu Asp Phe Leu Leu Ala Met
        115   120   125
Gln Tyr Glu Asn Gly Gly Phe Pro Gln Tyr Tyr Pro Leu Lys Asn Asp
    130   135   140
Tyr Ser Arg Glu Ile Thr Phe Asn Asp Asp Ala Met Ile Asn Val Leu
145   150   155   160
Lys Leu Leu Arg Asp Val Ala Lys Lys Lys Glu Asp Tyr Leu Phe Val
                165   170   175
Asp Glu Asp Arg Arg Ala Arg Ala Glu Gly Ala Val Glu Lys Gly Val
            180   185   190
Arg Leu Ile Leu Lys Thr Gln Val Ala Ile Asp Gly Lys Lys Thr Ile
        195   200   205

Trp Ala Ala Gln Tyr Asp Glu Asn Thr Leu Lys Pro Ala Asn Ala Arg
210 215 220
Lys Phe Glu Pro Ala Ser Leu Ala Ser Arg Glu Ser Val Ser Val Val
225 230 235 240
Arg Phe Leu Met Leu Asp Ala Lys Pro Asp Glu Glu Lys Ile Gly Ala
245 250 255
Ile Glu Ser Ala Ile Glu Trp Phe Gln Lys Asn Lys Leu Ser Gly Ile
260 265 270
Arg Trp Glu Ser Lys Ser Gly Glu Asn Leu Val Val Lys Asp Lys Ala
275 280 285
Ala Pro Pro Ile Trp Gly Arg Phe Tyr Gln Phe Glu Thr Met Arg Pro
290 295 300
Ile Phe Ile Gly Arg Asp Ala Val Ile Arg Tyr Asp Val Met Gln Ile
305 310 315 320
Glu Ala Glu Arg Arg Asn Gly Tyr Gly Trp Tyr Thr Asn Glu Pro Asn
325 330 335
Glu Leu Leu Asp Lys Asp Tyr Pro Lys Trp Lys Glu Lys Ile Lys Lys
340 345 350
Asn

<210> 95
<211> 1074
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 95
atgacgctac ccgttgtttc cctgcgcgta ctgctggcgc tgctggccac gtcgccggtc
60
gcctgcgcgg gcgccgcggc acccgcgact gcgaccgatc cggtcgccga gaacatgctg
120
cttctgcaga ccgcctccgg cggctggtcc aagcactacc gcgagaagaa ggtcgactac
180
gcgcgcgact acgacgccgc cgagcgcgcc gcgctgcgcg cgcccgaccg gcatgacgat
240
gcgacgatcg acaacaaggc cacgaccacc gagatcgcct acctggtgca ggcacatgcc
300
aggacgggca atccggccta cctcgacggc gcgcgccgcg gcgtcgagta cctgctgcgc
360
gcccagtacc cgaacggcgg ctggccgcag ttctaccccg accattcgtc ctaccggcac
420
cagatcacgc tcaacgacga tgcgatggtg cacgccatca ccgtgctgca ggacatcgcc
480
gcgggccgca acggcatgca ggtgctggcg ccggagttcg gcgtccgcgc cgccgcggcc
540
gcgcagcgcg gcatcggaaa cctgctcgag ttgcaggtgc ggatcgccgg ggtgccgacg
600
atatgggccg cgcagtacga cgagaccagc ctgcaaccgg ccaaggcccg cgcgtacgaa
660
ctgccttcgc tggccgtggc cgaatcggtc ggcgtggtgc gcctgctgat gcgccagccg
720
gcgcctgatg cgcgcacggt cgccgcgatc gaggcggcgg ccgactggct ggaggcgcac
780
cgcctgccgg acctcgccct ggaacgcatc gaagcccccg ccgaggaaac cggcaaggac
840
gtccgcgtcg tggccagacc gggcgcgtcg ttgtgggcgc gcttctacga cctcgagcgg
900
caggtgccgc tgttcgtcga tcgcaacagc cgtccggtgc ccttcgccga gcttcccaac

960
gagcgtcgta ccggctatgg ctggtatggc acctggccgg aaaagctgct ggcacaggaa
1020
ctcccgcgct ggcgcaaggt ccatgcggcc agcgcgggcg ctccggcccg ttga
1074

<210> 96
<211> 357
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(31)

<221> DOMAIN
<222> (32)...(357)
<223> Catalytic domain

<400> 96
Met Thr Leu Pro Val Val Ser Leu Arg Val Leu Leu Ala Leu Leu Ala
 1   5   10   15
Thr Ser Pro Val Ala Cys Ala Gly Ala Ala Ala Pro Ala Thr Ala Thr
            20   25   30
Asp Pro Val Ala Glu Asn Met Leu Leu Leu Gln Thr Ala Ser Gly Gly
        35   40   45
Trp Ser Lys His Tyr Arg Glu Lys Lys Val Asp Tyr Ala Arg Asp Tyr
    50   55   60
Asp Ala Ala Glu Arg Ala Ala Leu Arg Ala Pro Asp Arg His Asp Asp
65   70   75   80
Ala Thr Ile Asp Asn Lys Ala Thr Thr Thr Glu Ile Ala Tyr Leu Val
                85   90   95
Gln Ala His Ala Arg Thr Gly Asn Pro Ala Tyr Leu Asp Gly Ala Arg
            100   105   110
Arg Gly Val Glu Tyr Leu Leu Arg Ala Gln Tyr Pro Asn Gly Gly Trp
        115   120   125
Pro Gln Phe Tyr Pro Asp His Ser Ser Tyr Arg His Gln Ile Thr Leu
    130   135   140
Asn Asp Asp Ala Met Val His Ala Ile Thr Val Leu Gln Asp Ile Ala
145   150   155   160
Ala Gly Arg Asn Gly Met Gln Val Leu Ala Pro Glu Phe Gly Val Arg
                165   170   175
Ala Ala Ala Ala Ala Gln Arg Gly Ile Gly Asn Leu Leu Glu Leu Gln
            180   185   190
Val Arg Ile Ala Gly Val Pro Thr Ile Trp Ala Ala Gln Tyr Asp Glu
        195   200   205
Thr Ser Leu Gln Pro Ala Lys Ala Arg Ala Tyr Glu Leu Pro Ser Leu
    210   215   220
Ala Val Ala Glu Ser Val Gly Val Val Arg Leu Leu Met Arg Gln Pro
225   230   235   240
Ala Pro Asp Ala Arg Thr Val Ala Ala Ile Glu Ala Ala Ala Asp Trp
                245   250   255
Leu Glu Ala His Arg Leu Pro Asp Leu Ala Leu Glu Arg Ile Glu Ala
            260   265   270
Pro Ala Glu Glu Thr Gly Lys Asp Val Arg Val Val Ala Arg Pro Gly
        275   280   285
Ala Ser Leu Trp Ala Arg Phe Tyr Asp Leu Glu Arg Gln Val Pro Leu
    290   295   300
Phe Val Asp Arg Asn Ser Arg Pro Val Pro Phe Ala Glu Leu Pro Asn

305 310 315 320
Glu Arg Arg Thr Gly Tyr Gly Trp Tyr Gly Thr Trp Pro Glu Lys Leu
325 330 335
Leu Ala Gln Glu Leu Pro Arg Trp Arg Lys Val His Ala Ala Ser Ala
340 345 350
Gly Ala Pro Ala Arg
355

<210> 97
<211> 2097
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 97
ttgaacgccg ccggcagccg gcggttcgcg caactcgtcg tcgcggatct gcggcggctg
60
gtgcccgcgc tggcgccctt ctttcgcgac gagccgctgg cgggaggagt cgccgcgctc
120
cagcgcagcg tcgatgcgat cgtcgccgcg gacggcaccg gacagtttgc gacggtgcag
180
gaggcgatca acgccgcgcc gcagaacacc agcacgacca gccgctggat catcctcgtc
240
aaaccaggca cgtatcgcga ggtcgtctac gtgcagcgtg agaagcgctt cgtcacgctg
300
atcggcgaag acccggcacg gacgacgatc acgtaccacc tcaaagcgtc tgacgtgggg
360
ctcgacggca agcccatcgg cacgtttcgc acgccgacga tggtggtgga tgccgacgat
420
ttcacgatcg agaacctcac catcgagaac ggggcagggc cggtcggtca agcgctggcc
480
ttgcgagtgg acggcgatcg cgtgacggtg aggaacagcc gcctgctggg ctggcaggac
540
acgatctttc tcaaccgtgg gcgccactac ttcgaggact cgttcatcgg cgggcacgtg
600
gatttcattt tcggcggcgc gacggcggtg ttcgagcgat gccatcttcg cgcctggcgg
660
gacggctacc tcacggccgc gtccacgccc gcggagcaac gattcggctt cgtgttcctg
720
aacagcatcg tcagtggaga agctggcgcc cgcacgtacc tcggtcgacc gtggcgggcg
780
ttcgcgcacg tggccttcat caagacgacg atgggcgagg tggtgcgccc ggtgggctgg
840
aacaactggg accggccgga gcgtgagaag accgtgcgtt ttctcgaagc aggcaccagc
900
ggcgcgggcg gcagcgtcgc tgcgcgcgtc gcctgggcgc gcgtcgccac gccagccgag
960
ctcgctgatc tgacgaccga ggtggtgctt ggcggcaccg acggctggga cccgcgtcgc
1020
gtcgccccgt acccgtcggc cgttcgcgcc aacgcggcgc cgctgccgcg gccgcccggg
1080
cccgacgtcg ctggcccgca gagcccgccc gccttgacgt gggaccaggt cgcgcgccag
1140
ccagcgtcgt ggctggccac acccgaagcg ctgcggattg ccgagaacgt gcgcctctat
1200
caacggcaca ctggcggctg gcccaaaaac ctcgacatgg cgcagccgtt gacggacgcc
1260
gatcgcgcgc gtctcacggc cgatcgcgcg ctcgacgact cgaccatcga caatggcgcc
1320

acgacgcggc agatcgagtt tctcgcccgg atcgccgccg ccaaccgcga cgagcgcgcg
1380
caggcgtcga tgctggctgg gatcgactac ctgctcgcgg cccagtatcc aaacggcggc
1440
tggccgcagt atttcccgct ccgcaacgac tactcgcgcc acatcacgtt caacgacgac
1500
gcgatgatcg cggccgcgac gatcctgcag tcggtcgcgc tggcccgtcc gccgttcgcc
1560
ggcgtcgacg cgactcgccg ccggcgggcg gcggaggccg tcgcgcgcgc ccatcgcgtg
1620
attctggcct cgcagattcg cgtcaacggc cagctcactg gctggtgcca gcagcacgat
1680
gcacgcacgc tggagccagc gcgcgggcgc acctacgagc atccatcgat cagtggccgc
1740
gaaaccgtga cgatcgtcaa tttcctgcgg tcgatcgaac cgcgcgaccg ccagacccaa
1800
gccgccatcg atgccgcgat ggagtggctc aaggccgtgc agatccgcgg ctggcgcacg
1860
gagcggcggc ccgatccctc aggaccgggc ggttacgacg tggtgatggt ggaggacccc
1920
aacgcggcgc cgctctgggc ccgcttctac gagattggca ccaatcgtcc gatctactcg
1980
ggccgggacg gcgtcatcaa gtaccggctc gccgagatcg aaattgaacg gcggaccggc
2040
tacagctggg tcggaccgta cgcgcaggcg ctgctcgatg aagagcgcag gaagtaa
2097

<210> 98
<211> 698
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (45)...(333)
<223> Pectin methyl esterase domain

<221> DOMAIN
<222> (336)...(698)
<223> Catalytic domain

<400> 98
Met Asn Ala Ala Gly Ser Arg Arg Phe Ala Gln Leu Val Val Ala Asp
 1   5   10   15
Leu Arg Arg Leu Val Pro Ala Leu Ala Pro Phe Phe Arg Asp Glu Pro
            20   25   30
Leu Ala Gly Gly Val Ala Ala Leu Gln Arg Ser Val Asp Ala Ile Val
        35   40   45
Ala Ala Asp Gly Thr Gly Gln Phe Ala Thr Val Gln Glu Ala Ile Asn
    50   55   60
Ala Ala Pro Gln Asn Thr Ser Thr Thr Ser Arg Trp Ile Ile Leu Val
65   70   75   80
Lys Pro Gly Thr Tyr Arg Glu Val Val Tyr Val Gln Arg Glu Lys Arg
                85   90   95
Phe Val Thr Leu Ile Gly Glu Asp Pro Ala Arg Thr Thr Ile Thr Tyr
            100   105   110
His Leu Lys Ala Ser Asp Val Gly Leu Asp Gly Lys Pro Ile Gly Thr
        115   120   125
Phe Arg Thr Pro Thr Met Val Val Asp Ala Asp Asp Phe Thr Ile Glu

```
    130                 135                 140
Asn Leu Thr Ile Glu Asn Gly Ala Gly Pro Val Gly Gln Ala Leu Ala
145                 150                 155                 160
Leu Arg Val Asp Gly Asp Arg Val Thr Val Arg Asn Ser Arg Leu Leu
                165                 170                 175
Gly Trp Gln Asp Thr Ile Phe Leu Asn Arg Gly Arg His Tyr Phe Glu
            180                 185                 190
Asp Ser Phe Ile Gly Gly His Val Asp Phe Ile Phe Gly Gly Ala Thr
        195                 200                 205
Ala Val Phe Glu Arg Cys His Leu Arg Ala Trp Arg Asp Gly Tyr Leu
    210                 215                 220
Thr Ala Ala Ser Thr Pro Ala Glu Gln Arg Phe Gly Phe Val Phe Leu
225                 230                 235                 240
Asn Ser Ile Val Ser Gly Glu Ala Gly Ala Arg Thr Tyr Leu Gly Arg
                245                 250                 255
Pro Trp Arg Ala Phe Ala His Val Ala Phe Ile Lys Thr Thr Met Gly
            260                 265                 270
Glu Val Val Arg Pro Val Gly Trp Asn Asn Trp Asp Arg Pro Glu Arg
        275                 280                 285
Glu Lys Thr Val Arg Phe Leu Glu Ala Gly Thr Ser Gly Ala Gly Gly
    290                 295                 300
Ser Val Ala Ala Arg Val Ala Trp Ala Arg Val Ala Thr Pro Ala Glu
305                 310                 315                 320
Leu Ala Asp Leu Thr Thr Glu Val Val Leu Gly Gly Thr Asp Gly Trp
                325                 330                 335
Asp Pro Arg Arg Val Ala Pro Tyr Pro Ser Ala Val Arg Ala Asn Ala
            340                 345                 350
Ala Pro Leu Pro Arg Pro Pro Gly Pro Asp Val Ala Gly Pro Gln Ser
        355                 360                 365
Pro Pro Ala Leu Thr Trp Asp Gln Val Ala Arg Gln Pro Ala Ser Trp
    370                 375                 380
Leu Ala Thr Pro Glu Ala Leu Arg Ile Ala Glu Asn Val Arg Leu Tyr
385                 390                 395                 400
Gln Arg His Thr Gly Gly Trp Pro Lys Asn Leu Asp Met Ala Gln Pro
                405                 410                 415
Leu Thr Asp Ala Asp Arg Ala Arg Leu Thr Ala Asp Arg Ala Leu Asp
            420                 425                 430
Asp Ser Thr Ile Asp Asn Gly Ala Thr Thr Arg Gln Ile Glu Phe Leu
        435                 440                 445
Ala Arg Ile Ala Ala Ala Asn Arg Asp Glu Arg Ala Gln Ala Ser Met
    450                 455                 460
Leu Ala Gly Ile Asp Tyr Leu Leu Ala Ala Gln Tyr Pro Asn Gly Gly
465                 470                 475                 480
Trp Pro Gln Tyr Phe Pro Leu Arg Asn Asp Tyr Ser Arg His Ile Thr
                485                 490                 495
Phe Asn Asp Asp Ala Met Ile Ala Ala Ala Thr Ile Leu Gln Ser Val
            500                 505                 510
Ala Leu Ala Arg Pro Pro Phe Ala Gly Val Asp Ala Thr Arg Arg Arg
        515                 520                 525
Arg Ala Ala Glu Ala Val Ala Arg Ala His Arg Val Ile Leu Ala Ser
    530                 535                 540
Gln Ile Arg Val Asn Gly Gln Leu Thr Gly Trp Cys Gln Gln His Asp
545                 550                 555                 560
Ala Arg Thr Leu Glu Pro Ala Arg Gly Arg Thr Tyr Glu His Pro Ser
                565                 570                 575
Ile Ser Gly Arg Glu Thr Val Thr Ile Val Asn Phe Leu Arg Ser Ile
            580                 585                 590
Glu Pro Arg Asp Arg Gln Thr Gln Ala Ala Ile Asp Ala Ala Met Glu
        595                 600                 605
Trp Leu Lys Ala Val Gln Ile Arg Gly Trp Arg Thr Glu Arg Arg Pro
    610                 615                 620
```

Asp Pro Ser Gly Pro Gly Gly Tyr Asp Val Val Met Val Glu Asp Pro
625 630 635 640
Asn Ala Ala Pro Leu Trp Ala Arg Phe Tyr Glu Ile Gly Thr Asn Arg
645 650 655
Pro Ile Tyr Ser Gly Arg Asp Gly Val Ile Lys Tyr Arg Leu Ala Glu
660 665 670
Ile Glu Ile Glu Arg Arg Thr Gly Tyr Ser Trp Val Gly Pro Tyr Ala
675 680 685
Gln Ala Leu Leu Asp Glu Glu Arg Arg Lys
690 695

<210> 99
<211> 1782
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 99
atgttcacta ctaacagctc tatttgcgcc cggaaatccg cgcgtttttc actgactgcc
60
atggctgctg cggtggctat gatcgcgggc acctctgcct ttgcggcctc taccggtggc
120
ttttcgacca cggatggcgg caatgtgtca gggtcaaaat cctttaccgc ctcaagccac
180
acccaaatcc agcaaatcct tgaggatgcc aaagatggca attatccggt ggtgatcacc
240
tacaccggca atgaggattc actgattaac caagtcgtcc gggatcacac cgtcgattct
300
tcaggcaact gccctaaagc gcgttggaat gatgcctacc gcaaagtcga aatcaaagaa
360
atgaccaagg gtgtcaccat tcagggtgcc aatggttcgt cggcgaattt cggaatcgtg
420
gtgaataaat ccagcaacgt gattattcgc aacatgaaga ttggtgcact gggcggcgct
480
aataacgatg cggatatgat ccgtgtggac agcggtgtga acgtctggat cgatcacaac
540
gaattattcg ccgtgaacaa cgagtgtaag ggttcacccg atggcgatct gacctttgaa
600
agcgcgattg atatcaaaaa agcctcgcaa gatatcaccg tgtcctacaa cgtgattcgc
660
gacagtaaaa aagtcggttt ggatggctcc agcagcagcg atatcgccgg cggccgcaaa
720
attactttcc accacaatat ctaccgcaac gtaggtgcgc gcttaccttt gcagcgcggc
780
ggttggacgc acatgtacaa caacctgtac gacggcatta ccagctcggg catcaacgtg
840
cgccaaaacg gttatgcgtt aattgaaagc aactggttcc aaaacgcggt taacccggtc
900
acctgccgtt ttgacagcag caactgcggc aagtgggatc tgcgcaacaa taacatccgc
960
aacccgggtg attttgcgac ttacaacatc acctggacca gtggcggcac catcgacgcc
1020
accaactgga ccaccactgc gcccttccct atcagcattc cctacagcta ttcaccggtt
1080
actccgcaat gtgtgaaaga tcgtctggcg agttacgcgg gtgtgggtaa aaacggcgcg
1140
cagctgactg cctcggcctg cggtggtgcg gcatcgtcca cacctgcatc gtccacacct
1200
gcaagttcca gctctgcggc aaacagttcc gctgcatcag gcagtgtgag tttgggtggc

1260
agtgccggta atgcatcggt tgcacttaac tggaccgtga atgccaacat taatgcgctg
1320
gaaatttatc aggatacgga ttctgatccc gccggacgtg tgcgcattgc gtcgctgcca
1380
accagcgcga ccaactacac cgcaacaggt ctgagcaacg gcactaccta ttacttctgg
1440
gtgaaatatc gcaccaccaa taatgtgtgg agcaactcca atgtgttcag cgccaagcca
1500
agttcaggta caaccccgtc atcatccagc agcgcggctt catcaacgcc aagtggtgca
1560
ccggtgttaa gtggtacagg tgattaccca agcggcttct ccaagtgtgc tgatctgggt
1620
ggcacctgct cagtcgcctc gggcgatggt tgggttgcct ttggtcgcaa aggcaagtgg
1680
gtcaccaaaa aagtgtcagt cggtagctct attgcctgta ccgttgccgc gtttggatct
1740
gatccacaag gcaatcccaa taagtgttct tataaaaagt aa
1782

<210> 100
<211> 593
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(35)

<221> DOMAIN
<222> (36)...(593)
<223> Catalytic domain

<400> 100
Met Phe Thr Thr Asn Ser Ser Ile Cys Ala Arg Lys Ser Ala Arg Phe
 1   5   10   15
Ser Leu Thr Ala Met Ala Ala Ala Val Ala Met Ile Ala Gly Thr Ser
            20   25   30
Ala Phe Ala Ala Ser Thr Gly Gly Phe Ser Thr Thr Asp Gly Gly Asn
        35   40   45
Val Ser Gly Ser Lys Ser Phe Thr Ala Ser Ser His Thr Gln Ile Gln
    50   55   60
Gln Ile Leu Glu Asp Ala Lys Asp Gly Asn Tyr Pro Val Val Ile Thr
65   70   75   80
Tyr Thr Gly Asn Glu Asp Ser Leu Ile Asn Gln Val Val Arg Asp His
                85   90   95
Thr Val Asp Ser Ser Gly Asn Cys Pro Lys Ala Arg Trp Asn Asp Ala
            100   105   110
Tyr Arg Lys Val Glu Ile Lys Glu Met Thr Lys Gly Val Thr Ile Gln
        115   120   125
Gly Ala Asn Gly Ser Ser Ala Asn Phe Gly Ile Val Val Asn Lys Ser
    130   135   140
Ser Asn Val Ile Ile Arg Asn Met Lys Ile Gly Ala Leu Gly Gly Ala
145   150   155   160
Asn Asn Asp Ala Asp Met Ile Arg Val Asp Ser Gly Val Asn Val Trp
                165   170   175
Ile Asp His Asn Glu Leu Phe Ala Val Asn Asn Glu Cys Lys Gly Ser
            180   185   190
Pro Asp Gly Asp Leu Thr Phe Glu Ser Ala Ile Asp Ile Lys Lys Ala

```
        195                 200                 205
Ser Gln Asp Ile Thr Val Ser Tyr Asn Val Ile Arg Asp Ser Lys Lys
    210                 215                 220
Val Gly Leu Asp Gly Ser Ser Ser Ser Asp Ile Ala Gly Gly Arg Lys
225                 230                 235                 240
Ile Thr Phe His His Asn Ile Tyr Arg Asn Val Gly Ala Arg Leu Pro
                245                 250                 255
Leu Gln Arg Gly Gly Trp Thr His Met Tyr Asn Asn Leu Tyr Asp Gly
            260                 265                 270
Ile Thr Ser Ser Gly Ile Asn Val Arg Gln Asn Gly Tyr Ala Leu Ile
        275                 280                 285
Glu Ser Asn Trp Phe Gln Asn Ala Val Asn Pro Val Thr Cys Arg Phe
    290                 295                 300
Asp Ser Ser Asn Cys Gly Lys Trp Asp Leu Arg Asn Asn Asn Ile Arg
305                 310                 315                 320
Asn Pro Gly Asp Phe Ala Thr Tyr Asn Ile Thr Trp Thr Ser Gly Gly
                325                 330                 335
Thr Ile Asp Ala Thr Asn Trp Thr Thr Thr Ala Pro Phe Pro Ile Ser
            340                 345                 350
Ile Pro Tyr Ser Tyr Ser Pro Val Thr Pro Gln Cys Val Lys Asp Arg
        355                 360                 365
Leu Ala Ser Tyr Ala Gly Val Gly Lys Asn Gly Ala Gln Leu Thr Ala
    370                 375                 380
Ser Ala Cys Gly Gly Ala Ala Ser Ser Thr Pro Ala Ser Ser Thr Pro
385                 390                 395                 400
Ala Ser Ser Ser Ser Ala Ala Asn Ser Ser Ala Ala Ser Gly Ser Val
                405                 410                 415
Ser Leu Gly Gly Ser Ala Gly Asn Ala Ser Val Ala Leu Asn Trp Thr
            420                 425                 430
Val Asn Ala Asn Ile Asn Ala Leu Glu Ile Tyr Gln Asp Thr Asp Ser
        435                 440                 445
Asp Pro Ala Gly Arg Val Arg Ile Ala Ser Leu Pro Thr Ser Ala Thr
    450                 455                 460
Asn Tyr Thr Ala Thr Gly Leu Ser Asn Gly Thr Thr Tyr Tyr Phe Trp
465                 470                 475                 480
Val Lys Tyr Arg Thr Thr Asn Asn Val Trp Ser Asn Ser Asn Val Phe
                485                 490                 495
Ser Ala Lys Pro Ser Ser Gly Thr Thr Pro Ser Ser Ser Ser Ser Ala
            500                 505                 510
Ala Ser Ser Thr Pro Ser Gly Ala Pro Val Leu Ser Gly Thr Gly Asp
        515                 520                 525
Tyr Pro Ser Gly Phe Ser Lys Cys Ala Asp Leu Gly Gly Thr Cys Ser
    530                 535                 540
Val Ala Ser Gly Asp Gly Trp Val Ala Phe Gly Arg Lys Gly Lys Trp
545                 550                 555                 560
Val Thr Lys Lys Val Ser Val Gly Ser Ser Ile Ala Cys Thr Val Ala
                565                 570                 575
Ala Phe Gly Ser Asp Pro Gln Gly Asn Pro Asn Lys Cys Ser Tyr Lys
            580                 585                 590
Lys
```

<210> 101
<211> 1404
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 101

atgactatag accgtcgaga attccttata gacctcatta tcggcaccgc cggcttcgca
60
atcgcaccga gtgatgcgtt cggccaagct gatccatgga aaaccgtcta tccgcaaatc
120
ctcgctcgca tacggccacc gaaatttccg aagcgagatt tcatcatcac tagattcggc
180
gcaaagccgg gaaccgacag cgccgctgcg atcgcaaaag ctatcaccgc gtgcagcaag
240
gcaggcggag gacgtgttct cgttcccgca ggagagtttc tcaccggagc gatccatctg
300
aaatcgaacg taaactttca cgtgtcaaaa ggcgcgacgc tgaaattctc gaccgacccg
360
aaggcatatc tcccgattgt acatacgcga tgggaaggaa tggagctgat gcatctgtca
420
ccgttcatct acgcttatga gcagacgaac atcgctatca cgggtcaggg aacgctcgac
480
ggccagggaa aatcattctt ctggaaatgg catggcaatc cggcttatgg cggcgatccg
540
aacacgctca gccaacggcc cgctcgtgcg cggctttacg agatgatgga taagaatgtg
600
ccggtcgccg aacgtgtctt cggtctcgga cattatctgc ggccgcagtt tattcagccg
660
tacaaatgca ggaacgtttt gatcgaagat gtgacgatcg tcgattcgcc gatgtgggaa
720
gttcatccgg tgctttgcga gaacgtcacg gtccgaaatg ttcacatttc atcgcatggt
780
ccgaacaatg acggatgcga tccggagtcg tgcaaggacg tactgatcga caactgtttt
840
ttcgacaccg gcgacgattg catcgcgatc aagtccggcc gcaacaatga cggtcgtcgg
900
atcaatgtcc cgaccgagaa catcatcgtc cgcaactgca caatgaaaga cggtcatggc
960
ggcatcacgg tcggcagtga gatttcggga ggcgtgcgaa atctttttgc gcacgattgt
1020
cgactcgaca gtgcggatct ctggaccgcg cttcgcgtca agaacaatgc gtcgcgaggc
1080
ggcaagctcg agaattttta ttttcggaat ataacggtcg gccaggtcgc acgcgctgtg
1140
gtcgagatcg attttaatta cgaggaaggt gcgaaaggct cgtatattcc tgtcgttcga
1200
aattatgttg ttgaaggact gacatgcgcc acaggcaatc gcgccgtcga tctgcaagga
1260
ttggacaacg cgccgatcta caatgtaacg ctgcgaaact gtacgtttgg ttctgtccga
1320
aatcgtagtg ttgtgaaaaa cgttcgtgga cttcggctcg agaatgtgaa gatcggcggc
1380
aggatcgtaa acgaactggt atga
1404

<210> 102
<211> 467
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(28)

<221> DOMAIN

<222> (78)...(459)
<223> Catalytic domain

<400> 102

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Met Thr Ile Asp Arg Arg Glu Phe Leu Ile Asp Leu Ile Ile Gly Thr
 1               5                  10                  15
Ala Gly Phe Ala Ile Ala Pro Ser Asp Ala Phe Gly Gln Ala Asp Pro
            20                  25                  30
Trp Lys Thr Val Tyr Pro Gln Ile Leu Ala Arg Ile Arg Pro Pro Lys
        35                  40                  45
Phe Pro Lys Arg Asp Phe Ile Ile Thr Arg Phe Gly Ala Lys Pro Gly
    50                  55                  60
Thr Asp Ser Ala Ala Ala Ile Ala Lys Ala Ile Thr Ala Cys Ser Lys
65                  70                  75                  80
Ala Gly Gly Gly Arg Val Leu Val Pro Ala Gly Glu Phe Leu Thr Gly
                85                  90                  95
Ala Ile His Leu Lys Ser Asn Val Asn Phe His Val Ser Lys Gly Ala
            100                 105                 110
Thr Leu Lys Phe Ser Thr Asp Pro Lys Ala Tyr Leu Pro Ile Val His
        115                 120                 125
Thr Arg Trp Glu Gly Met Glu Leu Met His Leu Ser Pro Phe Ile Tyr
    130                 135                 140
Ala Tyr Glu Gln Thr Asn Ile Ala Ile Thr Gly Gln Gly Thr Leu Asp
145                 150                 155                 160
Gly Gln Gly Lys Ser Phe Phe Trp Lys Trp His Gly Asn Pro Ala Tyr
                165                 170                 175
Gly Gly Asp Pro Asn Thr Leu Ser Gln Arg Pro Ala Arg Ala Arg Leu
            180                 185                 190
Tyr Glu Met Met Asp Lys Asn Val Pro Val Ala Glu Arg Val Phe Gly
        195                 200                 205
Leu Gly His Tyr Leu Arg Pro Gln Phe Ile Gln Pro Tyr Lys Cys Arg
    210                 215                 220
Asn Val Leu Ile Glu Asp Val Thr Ile Val Asp Ser Pro Met Trp Glu
225                 230                 235                 240
Val His Pro Val Leu Cys Glu Asn Val Thr Val Arg Asn Val His Ile
                245                 250                 255
Ser Ser His Gly Pro Asn Asn Asp Gly Cys Asp Pro Glu Ser Cys Lys
            260                 265                 270
Asp Val Leu Ile Asp Asn Cys Phe Phe Asp Thr Gly Asp Asp Cys Ile
        275                 280                 285
Ala Ile Lys Ser Gly Arg Asn Asn Asp Gly Arg Arg Ile Asn Val Pro
    290                 295                 300
Thr Glu Asn Ile Ile Val Arg Asn Cys Thr Met Lys Asp Gly His Gly
305                 310                 315                 320
Gly Ile Thr Val Gly Ser Glu Ile Ser Gly Gly Val Arg Asn Leu Phe
                325                 330                 335
Ala His Asp Cys Arg Leu Asp Ser Ala Asp Leu Trp Thr Ala Leu Arg
            340                 345                 350
Val Lys Asn Asn Ala Ser Arg Gly Gly Lys Leu Glu Asn Phe Tyr Phe
        355                 360                 365
Arg Asn Ile Thr Val Gly Gln Val Ala Arg Ala Val Val Glu Ile Asp
    370                 375                 380
Phe Asn Tyr Glu Glu Gly Ala Lys Gly Ser Tyr Ile Pro Val Val Arg
385                 390                 395                 400
Asn Tyr Val Val Glu Gly Leu Thr Cys Ala Thr Gly Asn Arg Ala Val
                405                 410                 415
Asp Leu Gln Gly Leu Asp Asn Ala Pro Ile Tyr Asn Val Thr Leu Arg
            420                 425                 430
Asn Cys Thr Phe Gly Ser Val Arg Asn Arg Ser Val Val Lys Asn Val
        435                 440                 445
Arg Gly Leu Arg Leu Glu Asn Val Lys Ile Gly Gly Arg Ile Val Asn
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450 455 460
Glu Leu Val
465

<210> 103
<211> 1101
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 103
atgaacaccg cactgcaccg cgtcatccgc ctgccgctgc tgctggcgct gtgcctgccc
60
gcgctgcagg cacaggccac gcagaccgag cccgtcgccg agaacatgct gctgctgcag
120
accgcgtccg gcggctggtc caagcaccac cagggcaagg cggtcgacta cggccacacg
180
ttcaccgatg ccgaacgtgc ggcgctgcgc gcgcccgacc gcagggacga tgcgacgatc
240
gacaacaagg cgaccacgct tgagatcgtc gcgctgctgg aagcccacca gcgcaccggc
300
aatgccgcct atctggcggc tgcgcagcgc ggcgtggact acctgctggc cgcgcagtac
360
ccgaacggcg gctggccgca gtactacccg gaccgttcgc tgtaccggca ccaggtcacc
420
ttcaacgatg atgcgatgac ccgcgtgctg gagctgctgc aggacatcgt cgagggcaag
480
ggcgcgctgg cgcagctgac acccacgcat ggcgaacgcg ccagggccgc gctcgacagg
540
ggcatcgcct gcgtgctcgc cacccaggta cggatcgatg gcgagctcac gctctgggcc
600
gcgcagtacg acgaagccac gctgcagccg gcgaaggcgc gctcctacga gctgccatcg
660
ctggcggtcg ccgaatcggt cggggtgatg cggctgctga tgcgccagcc acagccgtcg
720
ccgcaggtgc tgacggcggt cgaggccggc gcacgctggc tggaggcgca ccgcatgcgc
780
gacctggccc ggcgaaagat cgacgcgccc ggcgaagaaa ccggccagga cgtggtgatc
840
gtcgccgagc ccggcgcgtc gctgtgggca cgcttctacg acctgcagca ccagcagccg
900
atgttcgtga accgcgaagg cgagcaggtg gcccgcttcg ccgacatgcc caacgaacgc
960
cgcgtcggct acgcctggta tggcgtgtgg ccggagaagc tgctgcagca ggagctgcca
1020
cgctggtaca acacccatgc cgaggcattg cgcgcgatta cgcctgcgca tgccgagcca
1080
aggccgccga agcggccctg a
1101

<210> 104
<211> 366
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(26)

<221> DOMAIN
<222> (27)...(366)
<223> Catalytic domain

<400> 104
Met Asn Thr Ala Leu His Arg Val Ile Arg Leu Pro Leu Leu Leu Ala
 1   5   10   15
Leu Cys Leu Pro Ala Leu Gln Ala Gln Ala Thr Gln Thr Glu Pro Val
            20   25   30
Ala Glu Asn Met Leu Leu Leu Gln Thr Ala Ser Gly Gly Trp Ser Lys
        35   40   45
His His Gln Gly Lys Ala Val Asp Tyr Gly His Thr Phe Thr Asp Ala
    50   55   60
Glu Arg Ala Ala Leu Arg Ala Pro Asp Arg Arg Asp Asp Ala Thr Ile
65   70   75   80
Asp Asn Lys Ala Thr Thr Leu Glu Ile Val Ala Leu Leu Glu Ala His
                85   90   95
Gln Arg Thr Gly Asn Ala Ala Tyr Leu Ala Ala Ala Gln Arg Gly Val
            100   105   110
Asp Tyr Leu Leu Ala Ala Gln Tyr Pro Asn Gly Gly Trp Pro Gln Tyr
        115   120   125
Tyr Pro Asp Arg Ser Leu Tyr Arg His Gln Val Thr Phe Asn Asp Asp
    130   135   140
Ala Met Thr Arg Val Leu Glu Leu Leu Gln Asp Ile Val Glu Gly Lys
145   150   155   160
Gly Ala Leu Ala Gln Leu Thr Pro Thr His Gly Glu Arg Ala Arg Ala
                165   170   175
Ala Leu Asp Arg Gly Ile Ala Cys Val Leu Ala Thr Gln Val Arg Ile
            180   185   190
Asp Gly Glu Leu Thr Leu Trp Ala Ala Gln Tyr Asp Glu Ala Thr Leu
        195   200   205
Gln Pro Ala Lys Ala Arg Ser Tyr Glu Leu Pro Ser Leu Ala Val Ala
    210   215   220
Glu Ser Val Gly Val Met Arg Leu Leu Met Arg Gln Pro Gln Pro Ser
225   230   235   240
Pro Gln Val Leu Thr Ala Val Glu Ala Gly Ala Arg Trp Leu Glu Ala
                245   250   255
His Arg Met Arg Asp Leu Ala Arg Arg Lys Ile Asp Ala Pro Gly Glu
            260   265   270
Glu Thr Gly Gln Asp Val Val Ile Val Ala Glu Pro Gly Ala Ser Leu
        275   280   285
Trp Ala Arg Phe Tyr Asp Leu Gln His Gln Gln Pro Met Phe Val Asn
    290   295   300
Arg Glu Gly Glu Gln Val Ala Arg Phe Ala Asp Met Pro Asn Glu Arg
305   310   315   320
Arg Val Gly Tyr Ala Trp Tyr Gly Val Trp Pro Glu Lys Leu Leu Gln
                325   330   335
Gln Glu Leu Pro Arg Trp Tyr Asn Thr His Ala Glu Ala Leu Arg Ala
            340   345   350
Ile Thr Pro Ala His Ala Glu Pro Arg Pro Pro Lys Arg Pro
        355   360   365

<210> 105
<211> 1203
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 105
atgcaattca tcgaaacaca gcaattgggg accgccgcga aacccgtggc gggacgagga
60
ggcgacaggc gctttccgcg ggtcatgccc gccgtttgcg cgggccttgc cctcgccgtg
120
tcgtcggccg agccggtccg ggcgcagggc gcggatgcgg atgcggatgg cccactgccc
180
aggtggaaca ggaggctggt ggatcgcccc gaggactggt tcgcctccga cgagggacag
240
cgcgttgccg ccaacgtcct ccgctaccaa tcggcggaag gagcctggcc caaaaacacc
300
aatctggccg ccactcccct tcgccccgag gacattccct cctcgacctc cggggtggcc
360
aacacgatcg acaatgaagc caccaccgtg cccattcggt ttttggcccg tttcgcgcaa
420
atcaacgagg acacggccag ccgcgaggcg gtccagcgcg gattggacta tctcctcaag
480
gcgcaatatc cgaacggtgg ctggccgcag tatttcccgc tccgccgcgg ctaccactcg
540
cacatcacct acaacgacga cgccatggtg aatgtgctcg acctgctgct ggacgtgtcg
600
ctgggcgagg agccgttcga ttttgtggac gaggatcgcc gccagcgggc cgcgaccgcc
660
gtggagcggg ggatcgaatg catcctccgc acccaaatcc ggcaggagga ccaacccacc
720
ggctggtgcg cgcagtatga ccccgaaacc ttggccccgg cgtggggacg ggcgtacgag
780
ccgccgtcga tttccggagc cgagaccgtc ggcgtggcgc ggtttctgat gcggctggag
840
tcgccatcgc cggaagccgt cgaagccatc gagggcgcca tcgcctggct cgacacggtg
900
ggcatcgagg aattgcgtct cgaatggttc accaacagcg agggcaagcg tgaccggcgc
960
gtggtcgagg acgcttccgt gggcaccctt tgggcgcgct tttacgaact cgaaacgaac
1020
cgccccttgt tcgtggaccg cgacggggtg ctccgctacg acttcgcgga actgacggcg
1080
gagcgccgcc aaggttacag ctactacggc acttggccgg cgccattgct ggccacggaa
1140
tatccgcgct ggcgcaggat gaacgagtcc gccctgctcg agtcgtcctt catctcgcat
1200
tga
1203

<210> 106
<211> 400
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(43)

<221> DOMAIN
<222> (44)...(400)
<223> Catalytic domain

<400> 106

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Met Gln Phe Ile Glu Thr Gln Gln Leu Gly Thr Ala Ala Lys Pro Val
 1               5                  10                  15
Ala Gly Arg Gly Gly Asp Arg Arg Phe Pro Arg Val Met Pro Ala Val
            20                  25                  30
Cys Ala Gly Leu Ala Leu Ala Val Ser Ser Ala Glu Pro Val Arg Ala
        35                  40                  45
Gln Gly Ala Asp Ala Asp Ala Asp Gly Pro Leu Pro Arg Trp Asn Arg
    50                  55                  60
Arg Leu Val Asp Arg Pro Glu Asp Trp Phe Ala Ser Asp Glu Gly Gln
65                  70                  75                  80
Arg Val Ala Ala Asn Val Leu Arg Tyr Gln Ser Ala Glu Gly Ala Trp
                85                  90                  95
Pro Lys Asn Thr Asn Leu Ala Ala Thr Pro Leu Arg Pro Glu Asp Ile
            100                 105                 110
Pro Ser Ser Thr Ser Gly Val Ala Asn Thr Ile Asp Asn Glu Ala Thr
        115                 120                 125
Thr Val Pro Ile Arg Phe Leu Ala Arg Phe Ala Gln Ile Asn Glu Asp
    130                 135                 140
Thr Ala Ser Arg Glu Ala Val Gln Arg Gly Leu Asp Tyr Leu Leu Lys
145                 150                 155                 160
Ala Gln Tyr Pro Asn Gly Gly Trp Pro Gln Tyr Phe Pro Leu Arg Arg
                165                 170                 175
Gly Tyr His Ser His Ile Thr Tyr Asn Asp Asp Ala Met Val Asn Val
            180                 185                 190
Leu Asp Leu Leu Leu Asp Val Ser Leu Gly Glu Glu Pro Phe Asp Phe
        195                 200                 205
Val Asp Glu Asp Arg Arg Gln Arg Ala Ala Thr Ala Val Glu Arg Gly
    210                 215                 220
Ile Glu Cys Ile Leu Arg Thr Gln Ile Arg Gln Glu Asp Gln Pro Thr
225                 230                 235                 240
Gly Trp Cys Ala Gln Tyr Asp Pro Glu Thr Leu Ala Pro Ala Trp Gly
                245                 250                 255
Arg Ala Tyr Glu Pro Pro Ser Ile Ser Gly Ala Glu Thr Val Gly Val
            260                 265                 270
Ala Arg Phe Leu Met Arg Leu Glu Ser Pro Ser Pro Glu Ala Val Glu
        275                 280                 285
Ala Ile Glu Gly Ala Ile Ala Trp Leu Asp Thr Val Gly Ile Glu Glu
    290                 295                 300
Leu Arg Leu Glu Trp Phe Thr Asn Ser Glu Gly Lys Arg Asp Arg Arg
305                 310                 315                 320
Val Val Glu Asp Ala Ser Val Gly Thr Leu Trp Ala Arg Phe Tyr Glu
                325                 330                 335
Leu Glu Thr Asn Arg Pro Leu Phe Val Asp Arg Asp Gly Val Leu Arg
            340                 345                 350
Tyr Asp Phe Ala Glu Leu Thr Ala Glu Arg Arg Gln Gly Tyr Ser Tyr
        355                 360                 365
Tyr Gly Thr Trp Pro Ala Pro Leu Leu Ala Thr Glu Tyr Pro Arg Trp
    370                 375                 380
Arg Arg Met Asn Glu Ser Ala Leu Leu Glu Ser Ser Phe Ile Ser His
385                 390                 395                 400
```

<210> 107
<211> 1074
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 107
atgacgctac ccgttgtttc cctgcgcgta ctgctggcgc tgctggccac gtcgccggtc

60
gcctgcgcgg gcgctgcggc acccgcgact gcgaccgatc cggtcgccga gaacatgctg
120
cttctgcaga ccgcctccgg cggctggtcc aagcactacc gcgagaagaa ggtcgactac
180
gcgcgcgact acgacgccgc cgagcgcgcc gcgctgcgcg cgcccgaccg gcatgacgat
240
gccacgatcg acaacaaggc cacgaccacc gagatcgcat acctggtgca ggcacatgcc
300
aggacgggca atccggccta cctcgacggc gcgcgccgcg gcgtcgagta cctgctgcgc
360
gcgcagtacc cgaacggcgg ctggccgcag ttctaccccg accattcgtc ctaccggcac
420
cagatcacgc tcaacgacga tgcgatggtg cacgccatca ccgtgctgca ggacatcgcc
480
gcgggccgca acggcatgca ggtgctggcg ccggagttcg gcgtccgcgc cgccgcggcc
540
gcgcagcgcg gcatcggaaa cctgctcgag ttgcaggtgc ggatcgacgg ggtgccgacg
600
atctgggccg cgcagtacga cgagaccacc ctgcaaccgg ccaaggcccg tgcgtacgag
660
ttgccctcgc tggccgtggc cgaatcggtg ggcgtgatgc gcctgctgat gcgccagccg
720
gggcctgatg cgcgcacgat cgccgcgatc gaggcggcgg cggactggct ggaggcgcac
780
cgcctgccgg acctcgccct ggaacgcatc gaagcccccg ccgaggaaac cggcaaggac
840
gtccgcgtcg tggccagacc gggcgcgtcg ttgtgggcgc gcttctacga cctcgagcgg
900
caggtgccgc tgttcgtcga tcgcaacagc cgtccggttc cattcgccga gcttcccaac
960
gagcgtcgta ccggctatgg ctggtatggc acctggccgg aaaagctgct ggcacaggaa
1020
ctcccgcgct ggcgcaaggt ccatgcggcc agcgcgggcg ctccggcccg ttga
1074

<210> 108
<211> 357
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(31)

<221> DOMAIN
<222> (32)...(357)
<223> Catalytic domain

<400> 108
Met Thr Leu Pro Val Val Ser Leu Arg Val Leu Leu Ala Leu Leu Ala
 1   5   10   15
Thr Ser Pro Val Ala Cys Ala Gly Ala Ala Ala Pro Ala Thr Ala Thr
            20   25   30
Asp Pro Val Ala Glu Asn Met Leu Leu Leu Gln Thr Ala Ser Gly Gly
        35   40   45
Trp Ser Lys His Tyr Arg Glu Lys Lys Val Asp Tyr Ala Arg Asp Tyr
    50   55   60
Asp Ala Ala Glu Arg Ala Ala Leu Arg Ala Pro Asp Arg His Asp Asp

65 70 75 80
Ala Thr Ile Asp Asn Lys Ala Thr Thr Thr Glu Ile Ala Tyr Leu Val
85 90 95
Gln Ala His Ala Arg Thr Gly Asn Pro Ala Tyr Leu Asp Gly Ala Arg
100 105 110
Arg Gly Val Glu Tyr Leu Leu Arg Ala Gln Tyr Pro Asn Gly Gly Trp
115 120 125
Pro Gln Phe Tyr Pro Asp His Ser Ser Tyr Arg His Gln Ile Thr Leu
130 135 140
Asn Asp Asp Ala Met Val His Ala Ile Thr Val Leu Gln Asp Ile Ala
145 150 155 160
Ala Gly Arg Asn Gly Met Gln Val Leu Ala Pro Glu Phe Gly Val Arg
165 170 175
Ala Ala Ala Ala Ala Gln Arg Gly Ile Gly Asn Leu Leu Glu Leu Gln
180 185 190
Val Arg Ile Asp Gly Val Pro Thr Ile Trp Ala Ala Gln Tyr Asp Glu
195 200 205
Thr Thr Leu Gln Pro Ala Lys Ala Arg Ala Tyr Glu Leu Pro Ser Leu
210 215 220
Ala Val Ala Glu Ser Val Gly Val Met Arg Leu Leu Met Arg Gln Pro
225 230 235 240
Gly Pro Asp Ala Arg Thr Ile Ala Ala Ile Glu Ala Ala Ala Asp Trp
245 250 255
Leu Glu Ala His Arg Leu Pro Asp Leu Ala Leu Glu Arg Ile Glu Ala
260 265 270
Pro Ala Glu Glu Thr Gly Lys Asp Val Arg Val Val Ala Arg Pro Gly
275 280 285
Ala Ser Leu Trp Ala Arg Phe Tyr Asp Leu Glu Arg Gln Val Pro Leu
290 295 300
Phe Val Asp Arg Asn Ser Arg Pro Val Pro Phe Ala Glu Leu Pro Asn
305 310 315 320
Glu Arg Arg Thr Gly Tyr Gly Trp Tyr Gly Thr Trp Pro Glu Lys Leu
325 330 335
Leu Ala Gln Glu Leu Pro Arg Trp Arg Lys Val His Ala Ala Ser Ala
340 345 350
Gly Ala Pro Ala Arg
355

<210> 109
<211> 1422
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 109
atgacgacac gacgcgaatt catcaaaggc tttctactta ccggagcagc cgtggccgtc
60
gctccgcgtt tgcttgcgtt cgccgcggag gcaagtccgt gggaaacgat gatgccttcg
120
atcctcgcac gcatcagacc acctcgtttt ccgaaacgca ccttctatct caatcgattc
180
ggcgccaagg gtgatggagt cacagactgc accgcggctt ttcatcgcgc gatcgatgaa
240
tgcaccaaag ccggcggtgg gaaagtcgtc gtgccggcgg gcacttatct caccggcgcg
300
attcatttga agagcaacgt caacctcgaa gtctcggaag gcgcgacgat caagttcagt
360
caggacccga aacactacct gcctgttgtc ttctcgcgtt gggaaggtgt cgaagtcttc
420

aactactcgc ctttcattta cgcgttcgaa cagcgaaaca tcgcgatcac cggcaaaggc
480
acgctcgacg gacagagtga ttcggaacac tggtggccgt ggaacggccg tccgcagtac
540
ggatggaaag aagggatgaa acagcagcgt cccgatcgca acgcgttgtt cacaatggcg
600
gagaaaggcg tgccggtgcg cgagcgcatc tttggcgaag gtcattattt gaggccgcag
660
ttcattcagc cgtaccgctg ccagaacgtg ctgatccagg gcgtgacgat tcggaactcg
720
ccgatgtggg agattcatcc ggtgttgtgc cgtaacgtga ctattcacga cgtgcacatc
780
gatagtcatg gaccaaacaa cgacggctgc aatcccgaat cgtgcagcga cgtgttgatt
840
aaggatagct acttcgatac cggcgacgac tgcatcgcga tcaaatcggg acgcaacgcc
900
gacgggcggc ggcttaaagc gccgactgag aacatcatcg ttcaaggatg tcgcatgaaa
960
gacggccacg gtggaatcac ggtcggcagc gagatctcgg gcggcgtgcg aaacctgttt
1020
gccgagaatt gccggctcga cagtccaaac ctcgatcacg ccctgcgcgt gaagaacaat
1080
gccatgcgcg gcggattact cgagaacttc cacttccgta acatcgaagt cgggcaggtg
1140
gcccatgccg tgattacgat cgacttcaac tacgaagagg gcgcgaaagg gtcgttcacg
1200
ccggtcgttc gcgattacac ggtcgatcgt ttgcgcagca cgaagagcaa gcacgcactc
1260
gacgtccagg gtctgcccgg cgcgccggtc atcaacctgc gattgacgaa ctgcacattc
1320
aacgatgtgc agcaaccgaa cattctcaag aacgtcgaac aatcaacctt tgaaaacgtc
1380
acgattaacg gaaagacgat cacacaaaca ggatccaaag aa
1422

<210> 110
<211> 474
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(21)

<221> DOMAIN
<222> (28)...(308)
<223> Pectin methyl esterase domain

<221> DOMAIN
<222> (309)...(637)
<223> Catalytic domain

<400> 110
Met Thr Thr Arg Arg Glu Phe Ile Lys Gly Phe Leu Leu Thr Gly Ala
 1   5   10   15
Ala Val Ala Val Ala Pro Arg Leu Leu Ala Phe Ala Ala Glu Ala Ser
            20   25   30
Pro Trp Glu Thr Met Met Pro Ser Ile Leu Ala Arg Ile Arg Pro Pro
        35   40   45

```
Arg Phe Pro Lys Arg Thr Phe Tyr Leu Asn Arg Phe Gly Ala Lys Gly
    50                  55                  60
Asp Gly Val Thr Asp Cys Thr Ala Ala Phe His Arg Ala Ile Asp Glu
65                  70                  75                  80
Cys Thr Lys Ala Gly Gly Gly Lys Val Val Val Pro Ala Gly Thr Tyr
                85                  90                  95
Leu Thr Gly Ala Ile His Leu Lys Ser Asn Val Asn Leu Glu Val Ser
            100                 105                 110
Glu Gly Ala Thr Ile Lys Phe Ser Gln Asp Pro Lys His Tyr Leu Pro
        115                 120                 125
Val Val Phe Ser Arg Trp Glu Gly Val Glu Val Phe Asn Tyr Ser Pro
    130                 135                 140
Phe Ile Tyr Ala Phe Glu Gln Arg Asn Ile Ala Ile Thr Gly Lys Gly
145                 150                 155                 160
Thr Leu Asp Gly Gln Ser Asp Ser Glu His Trp Trp Pro Trp Asn Gly
                165                 170                 175
Arg Pro Gln Tyr Gly Trp Lys Glu Gly Met Lys Gln Gln Arg Pro Asp
            180                 185                 190
Arg Asn Ala Leu Phe Thr Met Ala Glu Lys Gly Val Pro Val Arg Glu
        195                 200                 205
Arg Ile Phe Gly Glu Gly His Tyr Leu Arg Pro Gln Phe Ile Gln Pro
    210                 215                 220
Tyr Arg Cys Gln Asn Val Leu Ile Gln Gly Val Thr Ile Arg Asn Ser
225                 230                 235                 240
Pro Met Trp Glu Ile His Pro Val Leu Cys Arg Asn Val Thr Ile His
                245                 250                 255
Asp Val His Ile Asp Ser His Gly Pro Asn Asn Asp Gly Cys Asn Pro
            260                 265                 270
Glu Ser Cys Ser Asp Val Leu Ile Lys Asp Ser Tyr Phe Asp Thr Gly
        275                 280                 285
Asp Asp Cys Ile Ala Ile Lys Ser Gly Arg Asn Ala Asp Gly Arg Arg
    290                 295                 300
Leu Lys Ala Pro Thr Glu Asn Ile Ile Val Gln Gly Cys Arg Met Lys
305                 310                 315                 320
Asp Gly His Gly Gly Ile Thr Val Gly Ser Glu Ile Ser Gly Gly Val
                325                 330                 335
Arg Asn Leu Phe Ala Glu Asn Cys Arg Leu Asp Ser Pro Asn Leu Asp
            340                 345                 350
His Ala Leu Arg Val Lys Asn Asn Ala Met Arg Gly Gly Leu Leu Glu
        355                 360                 365
Asn Phe His Phe Arg Asn Ile Glu Val Gly Gln Val Ala His Ala Val
    370                 375                 380
Ile Thr Ile Asp Phe Asn Tyr Glu Glu Gly Ala Lys Gly Ser Phe Thr
385                 390                 395                 400
Pro Val Val Arg Asp Tyr Thr Val Asp Arg Leu Arg Ser Thr Lys Ser
                405                 410                 415
Lys His Ala Leu Asp Val Gln Gly Leu Pro Gly Ala Pro Val Ile Asn
            420                 425                 430
Leu Arg Leu Thr Asn Cys Thr Phe Asn Asp Val Gln Gln Pro Asn Ile
        435                 440                 445
Leu Lys Asn Val Glu Gln Ser Thr Phe Glu Asn Val Thr Ile Asn Gly
    450                 455                 460
Lys Thr Ile Thr Gln Thr Gly Ser Lys Glu
465                 470
```

<210> 111
<211> 1440
<212> DNA
<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 111
atgcaaaatc gtcgagaatt tttacaactt ttatttgccg gtgccggtgc cggacttgtt
60
ttgccgcaga tttctttcgg gcagactaaa caagccgacg cctggacgac cgagtatccg
120
aagattttag ccagaatcaa accgccgaaa tttcgcaaaa aagattttcc gatcaccaaa
180
tatggagccg ttgcggacgg gaaaaccctg gcgaccgaaa gcatcaaaaa agccatcgaa
240
gcgtgcgcca aatcgggcgg cgggcgcgtc gtcgtgcccc agggagaatt tttgaccggc
300
gcgattcatt tgaaatcaaa cgtcaatctg cacatcacga aaggcgcgac cgtcaaattt
360
tccaccaacc cgaaagatta tctgccgatc gttcacacgc gctgggaagg gatggaattg
420
atgcatattt cgcctttaat ttatgcctac gagcaaacca acatcgccgt caccggcgag
480
ggaacgctcg acgggcaggg caaggctttt ttctggaaat ggcacggaaa cccgcgctac
540
ggcggaaatc cggatgtgat cagccagcgt ccggcgcgcg cccggctgta tgaaatgatg
600
gaaaaaggcg tgcctgtggc ggagcggatt ttcggcgaaa ctcagtatct tcgcccgcag
660
tttatccagc cctataaatg caaaaatgtt ttgatcgaag gcgttaaaat catcgattcg
720
ccgatgtggg aagttcaccc cgttttgtgc gaaaacgtga cgatccgaaa acttcatatt
780
tctacccacg gaccgaacaa cgacgggtgc gatccggaaa gctgcaagga cgttttgatc
840
gaagactgct atttcgacac cggcgacgat tgcattgcca tcaaggcggg gcgcaatgaa
900
gacgggcgac gcatcaatgt tccgaccgaa aacgtcgtcg tgcgcgggtg cgtgatgaag
960
gacggtcacg gcggaatcac catcggaagc gagatttccg gcggcgtgcg aaatgttttc
1020
gcggaaaaca accggctcga cagcgcggat ttgtggactg cgctgagagt gaaaaacaac
1080
gcttcgcgcg gcggaaaact ggagaatttt tacttccgcg atatcaccgt cgggcaggtc
1140
tcgcgcgcgg tcgtcgaaat agattttaat tacgaggaag gcgctaaagg aaaacacacg
1200
ccggtcgttc gcaattacgt ggtcgaaaat ctaacctgca ataaaggcaa tcgagcggtc
1260
gatctgcagg gcttggacaa cgccccgatt tacgacatca cgatgaaaaa ctgtacgttt
1320
aacgtggtcg aaaagccgag cgtcgtgaaa aacgtcaaag gcgtcaaact ggaaaacgtg
1380
aagattaacg gcaaagtcgt cgagagtctg gaaaatgctg caacgacggc taaaaaataa
1440

<210> 112
<211> 479
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(27)

<221> DOMAIN
<222> (82)...(461)
<223> Catalytic domain

<400> 112

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Met Gln Asn Arg Arg Glu Phe Leu Gln Leu Leu Phe Ala Gly Ala Gly
 1               5                  10                  15
Ala Gly Leu Val Leu Pro Gln Ile Ser Phe Gly Gln Thr Lys Gln Ala
            20                  25                  30
Asp Ala Trp Thr Thr Glu Tyr Pro Lys Ile Leu Ala Arg Ile Lys Pro
        35                  40                  45
Pro Lys Phe Arg Lys Lys Asp Phe Pro Ile Thr Lys Tyr Gly Ala Val
    50                  55                  60
Ala Asp Gly Lys Thr Leu Ala Thr Glu Ser Ile Lys Lys Ala Ile Glu
65                  70                  75                  80
Ala Cys Ala Lys Ser Gly Gly Gly Arg Val Val Val Pro Gln Gly Glu
                85                  90                  95
Phe Leu Thr Gly Ala Ile His Leu Lys Ser Asn Val Asn Leu His Ile
            100                 105                 110
Thr Lys Gly Ala Thr Val Lys Phe Ser Thr Asn Pro Lys Asp Tyr Leu
        115                 120                 125
Pro Ile Val His Thr Arg Trp Glu Gly Met Glu Leu Met His Ile Ser
    130                 135                 140
Pro Leu Ile Tyr Ala Tyr Glu Gln Thr Asn Ile Ala Val Thr Gly Glu
145                 150                 155                 160
Gly Thr Leu Asp Gly Gln Gly Lys Ala Phe Phe Trp Lys Trp His Gly
                165                 170                 175
Asn Pro Arg Tyr Gly Gly Asn Pro Asp Val Ile Ser Gln Arg Pro Ala
            180                 185                 190
Arg Ala Arg Leu Tyr Glu Met Met Glu Lys Gly Val Pro Val Ala Glu
        195                 200                 205
Arg Ile Phe Gly Glu Thr Gln Tyr Leu Arg Pro Gln Phe Ile Gln Pro
    210                 215                 220
Tyr Lys Cys Lys Asn Val Leu Ile Glu Gly Val Lys Ile Ile Asp Ser
225                 230                 235                 240
Pro Met Trp Glu Val His Pro Val Leu Cys Glu Asn Val Thr Ile Arg
                245                 250                 255
Lys Leu His Ile Ser Thr His Gly Pro Asn Asn Asp Gly Cys Asp Pro
            260                 265                 270
Glu Ser Cys Lys Asp Val Leu Ile Glu Asp Cys Tyr Phe Asp Thr Gly
        275                 280                 285
Asp Asp Cys Ile Ala Ile Lys Ala Gly Arg Asn Glu Asp Gly Arg Arg
    290                 295                 300
Ile Asn Val Pro Thr Glu Asn Val Val Val Arg Gly Cys Val Met Lys
305                 310                 315                 320
Asp Gly His Gly Gly Ile Thr Ile Gly Ser Glu Ile Ser Gly Gly Val
                325                 330                 335
Arg Asn Val Phe Ala Glu Asn Asn Arg Leu Asp Ser Ala Asp Leu Trp
            340                 345                 350
Thr Ala Leu Arg Val Lys Asn Asn Ala Ser Arg Gly Gly Lys Leu Glu
        355                 360                 365
Asn Phe Tyr Phe Arg Asp Ile Thr Val Gly Gln Val Ser Arg Ala Val
    370                 375                 380
Val Glu Ile Asp Phe Asn Tyr Glu Glu Gly Ala Lys Gly Lys His Thr
385                 390                 395                 400
Pro Val Val Arg Asn Tyr Val Val Glu Asn Leu Thr Cys Asn Lys Gly
                405                 410                 415
Asn Arg Ala Val Asp Leu Gln Gly Leu Asp Asn Ala Pro Ile Tyr Asp
            420                 425                 430
```

Ile Thr Met Lys Asn Cys Thr Phe Asn Val Val Glu Lys Pro Ser Val
435 440 445
Val Lys Asn Val Lys Gly Val Lys Leu Glu Asn Val Lys Ile Asn Gly
450 455 460
Lys Val Val Glu Ser Leu Glu Asn Ala Ala Thr Thr Ala Lys Lys
465 470 475

<210> 113
<211> 1017
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 113
atgaagatat ttttaacaat attgctctcg gcattattca gcatttcaaa tgcacaggtg
60
ctatcggatc ctgttgcgga tcgtatgacc agctaccaac ttaaaaacgg aggctggccg
120
aagcacttgg ccgataaatc tgttgttaac tattcaaaac ctctctcacc tgctttgcaa
180
aaagtcatcg atcaatcgac cgaaaagtct gcgacaattg ataataatgc aaccacacgt
240
gagataaacc atcttctcct cgcttattcc aaaaccaaca atgacaagta tcttcaagcg
300
gcgacaaaag gtgttgagta tatcctgagt gctcaaaatg acaaaggagg atggcctcaa
360
tattatccag acagtagctc atatcgtggt cagatcacct acaatgacgg cgcgatgatt
420
aatgtattgg aaatttttact ttccatatca acaaaacaag agccctatgc tgttctaacg
480
aataaattta acgaaagaat agaaagggcc ttaacacgag ggattcactg catcttacaa
540
acccaggtta aacaaggaga taaactaacc atctgggccg cacagtacga tcagaaaaca
600
atggaacctg ctcaagccag actgtttgaa ccggtagcgt tagcgacagc ggaatcggcg
660
ggcattctcc gctttttaat gcgtcttgac catcctactc ccgaaataaa aaatgcaatc
720
aaccacgctg tagaatggtt ttcctcccat aaagaggtag gctatgatta cgttaaaacg
780
gaaaaaaacg gaaaactttt gcgggatttg gtttcttcgc cggcctctac cgtatgggca
840
agattttatg acatcaggac gaatcaaccc atctttggtg atcgcgataa tacgataaag
900
tattcgctga atgaaataag cgaggaacga caaaatggct actcttggta tggtaactgg
960
ccagaaaaga taattacaaa agaatatgaa aaatggctta agaaggtaaa tgaataa
1017

<210> 114
<211> 338
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> SIGNAL
<222> (1)...(18)

<221> DOMAIN
<222> (19)...(388)
<223> Catalytic domain

<400> 114
Met Lys Ile Phe Leu Thr Ile Leu Leu Ser Ala Leu Phe Ser Ile Ser
 1   5   10   15
Asn Ala Gln Val Leu Ser Asp Pro Val Ala Asp Arg Met Thr Ser Tyr
            20   25   30
Gln Leu Lys Asn Gly Gly Trp Pro Lys His Leu Ala Asp Lys Ser Val
        35   40   45
Val Asn Tyr Ser Lys Pro Leu Ser Pro Ala Leu Gln Lys Val Ile Asp
    50   55   60
Gln Ser Thr Glu Lys Ser Ala Thr Ile Asp Asn Asn Ala Thr Thr Arg
65   70   75   80
Glu Ile Asn His Leu Leu Leu Ala Tyr Ser Lys Thr Asn Asn Asp Lys
                85   90   95
Tyr Leu Gln Ala Ala Thr Lys Gly Val Glu Tyr Ile Leu Ser Ala Gln
            100   105   110
Asn Asp Lys Gly Gly Trp Pro Gln Tyr Tyr Pro Asp Ser Ser Ser Tyr
        115   120   125
Arg Gly Gln Ile Thr Tyr Asn Asp Gly Ala Met Ile Asn Val Leu Glu
    130   135   140
Ile Leu Leu Ser Ile Ser Thr Lys Gln Glu Pro Tyr Ala Val Leu Thr
145   150   155   160
Asn Lys Phe Asn Glu Arg Ile Glu Arg Ala Leu Thr Arg Gly Ile His
                165   170   175
Cys Ile Leu Gln Thr Gln Val Lys Gln Gly Asp Lys Leu Thr Ile Trp
            180   185   190
Ala Ala Gln Tyr Asp Gln Lys Thr Met Glu Pro Ala Gln Ala Arg Leu
        195   200   205
Phe Glu Pro Val Ala Leu Ala Thr Ala Glu Ser Ala Gly Ile Leu Arg
    210   215   220
Phe Leu Met Arg Leu Asp His Pro Thr Pro Glu Ile Lys Asn Ala Ile
225   230   235   240
Asn His Ala Val Glu Trp Phe Ser Ser His Lys Glu Val Gly Tyr Asp
                245   250   255
Tyr Val Lys Thr Glu Lys Asn Gly Lys Leu Leu Arg Asp Leu Val Ser
            260   265   270
Ser Pro Ala Ser Thr Val Trp Ala Arg Phe Tyr Asp Ile Arg Thr Asn
        275   280   285
Gln Pro Ile Phe Gly Asp Arg Asp Asn Thr Ile Lys Tyr Ser Leu Asn
    290   295   300
Glu Ile Ser Glu Glu Arg Gln Asn Gly Tyr Ser Trp Tyr Gly Asn Trp
305   310   315   320
Pro Glu Lys Ile Ile Thr Lys Glu Tyr Glu Lys Trp Leu Lys Lys Val
                325   330   335
Asn Glu

<210> 115
<211> 996
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 115
gtggccaagg cgatcggcgg tccgttgccg ccggcaccag ggcagggatc gccggtaacg

60
tgggcgacga ttctccggca gccatcgccg tggtacgcgt ccgcggacgc gaaggcggtt
120
gccgaaaccg tgcgcgcgag ccagagagcc accggcggct ggccgaagaa cacggattgg
180
acggcgctcc agagcgacgc tgagcggcag gcgctgcgaa atgcccgcgc cgagaccgat
240
tcgacgatcg acaatggcgc cacggtcacc gagcttcgct ttctcacccg cgtgtatgtc
300
gccacgcgcg acgagctttt acgggaggcc gtgcttcgcg gcctcgacta cctgctggcg
360
tcgcagtaca gcaacggcgg ctggccacaa tactttccgt tgcggaccga ttactcgcgg
420
gacatcacgt tcaacgacga cgcgatgacc ggcgtggtgc tgctgctgaa ggatgccgcg
480
gacgggtcag caggtttcga attcgtcgac aaggcgagac gtgaccgcgc tgccgcggcc
540
gtgacgcgcg ccatcgcggt gatcctccgc acgcagattc gggtcaacgg tacgctgacc
600
ggctggtgcc agcagtacga cgccgacgcg ctgacgccgg cgcgcgggcg ctcgtacgag
660
catccgtcga ttgcgagccg cgagacggtc gggatcgcgc ggctgctgat gggcgtgccg
720
aatccgtcgc cagagatcgt ggctgccgtt gacgcggctg ccgcatggtt gggtaaatcg
780
gaactgaagg gtgtgcccga ggcgacggcg ccaggacttt gggcgcgctt ctacgacatc
840
gctacgaatc ggccgatcta ttcgggccgc gacggcgtca tcaagtaccg gctcgacgag
900
atcgagctcg agcggcgcac aggctacagc tgggttggcc cgtacgccgc ggcatttctg
960
acgaccgaat atccgaaatg gcgggcggca cgatga
996

<210> 116
<211> 331
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<221> DOMAIN
<222> (1)...(331)
<223> Catalytic domain

<400> 116
Met Ala Lys Ala Ile Gly Gly Pro Leu Pro Pro Ala Pro Gly Gln Gly
 1   5   10   15
Ser Pro Val Thr Trp Ala Thr Ile Leu Arg Gln Pro Ser Pro Trp Tyr
            20   25   30
Ala Ser Ala Asp Ala Lys Ala Val Ala Glu Thr Val Arg Ala Ser Gln
        35   40   45
Arg Ala Thr Gly Gly Trp Pro Lys Asn Thr Asp Trp Thr Ala Leu Gln
    50   55   60
Ser Asp Ala Glu Arg Gln Ala Leu Arg Asn Ala Arg Ala Glu Thr Asp
65   70   75   80
Ser Thr Ile Asp Asn Gly Ala Thr Val Thr Glu Leu Arg Phe Leu Thr
                85   90   95
Arg Val Tyr Val Ala Thr Arg Asp Glu Leu Leu Arg Glu Ala Val Leu
            100   105   110

Arg Gly Leu Asp Tyr Leu Leu Ala Ser Gln Tyr Ser Asn Gly Gly Trp
115 120 125
Pro Gln Tyr Phe Pro Leu Arg Thr Asp Tyr Ser Arg Asp Ile Thr Phe
130 135 140
Asn Asp Asp Ala Met Thr Gly Val Val Leu Leu Leu Lys Asp Ala Ala
145 150 155 160
Asp Gly Ser Ala Gly Phe Glu Phe Val Asp Lys Ala Arg Arg Asp Arg
165 170 175
Ala Ala Ala Ala Val Thr Arg Ala Ile Ala Val Ile Leu Arg Thr Gln
180 185 190
Ile Arg Val Asn Gly Thr Leu Thr Gly Trp Cys Gln Gln Tyr Asp Ala
195 200 205
Asp Ala Leu Thr Pro Ala Arg Gly Arg Ser Tyr Glu His Pro Ser Ile
210 215 220
Ala Ser Arg Glu Thr Val Gly Ile Ala Arg Leu Leu Met Gly Val Pro
225 230 235 240
Asn Pro Ser Pro Glu Ile Val Ala Ala Val Asp Ala Ala Ala Ala Trp
245 250 255
Leu Gly Lys Ser Glu Leu Lys Gly Val Pro Glu Ala Thr Ala Pro Gly
260 265 270
Leu Trp Ala Arg Phe Tyr Asp Ile Ala Thr Asn Arg Pro Ile Tyr Ser
275 280 285
Gly Arg Asp Gly Val Ile Lys Tyr Arg Leu Asp Glu Ile Glu Leu Glu
290 295 300
Arg Arg Thr Gly Tyr Ser Trp Val Gly Pro Tyr Ala Ala Ala Phe Leu
305 310 315 320
Thr Thr Glu Tyr Pro Lys Trp Arg Ala Ala Arg
325 330

<210> 117
<211> 1725
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 117
atgaagaatt ttgggtttgg taactacaag ttttttgtag cggcaatgtc tgtcgcgtct
60
ttttcgtatg cggcaagcta tacacccccg tcaacagcag tttcgaaaat caacagctat
120
cgaggctatt cggagctgac ttcagctgca tccggcatgg atatcgacca gtacacctac
180
aacatgacca cttggcaaat cgcaaacggc ggtttttaca aagccatggc cgacaagtat
240
aaaagcgcgt atggcggcgg tcaaaaatcc gaatggcaag ctaaaggcgg tggcgacctc
300
ggcactatag acaacaacgc caccatccag gaaatgcgtt tgctcgccgt gcgttacaaa
360
gaaacgacga acaacaatta caaatccgca tttaagacaa gtttcaacaa ggcggtcaat
420
tttcttttga ccatgcagcg ctccaaaggc ggactcccac aagtttggcc caaacgcggc
480
aactattctg accaaatcac gctaaatgac aacgccatga tccgcgccat ggtcacgatg
540
atggatatcg ccaacaagac gagtccattt gattcggata tcatcgacga cgccacccgc
600
agcaaaatga aatcggctct cgacaaagcg gtcgattact tgctcaaggc gcaaatcgtg
660
aacgacggaa aggtcacggt atggtgcgcc cagcacgaca ccaacagcct cgcccccgta

720
ggcgcacgag cctacgaact cccgagcaaa tccggcaacg aatccatggg cgttgtgtgg
780
tttttgatga actggccaga ccaaaacgaa gcaatccaga aggcggtcaa aggcgcaatc
840
gcttggtaca aaaagaataa actaaaagac aaggcgttta gcaagaccgc aggcgttgtg
900
gacaaggcgg gttcatcgct gtggttccgc ttttacgaag tcaacaacga caactacttt
960
ttctgcgacc gcgatggtgc tagcaccaag acgcaggact tcatgaaaat cagcgaagaa
1020
cgtcgcaagg gctaccagtg ggcaggcgat tacggctctg caattctagg caccgaaaat
1080
gcataccttg aagcactcgc caagatggac gacaactatg ttccacctcc gccagcacca
1140
gctatgtgcg gaaacgacac ttgcaaaacg tacatcgatg gcgttgactt tattgacatt
1200
caaggcgtca aggaaacaac caacacggga ttcgttggcg aaggttacgc caacgttgac
1260
aactccaccg gaagctatgt gacctacggc gtcaccgcat tcaaggaagg caaatacact
1320
ttgttcatca gctttgcaaa cggcggtggt tccgcacgcg gttacagcgt ttctgcagga
1380
gacaagacgt tacttgcaga cggcagcatg gaatctacag ccgcatggac cacttggaaa
1440
atgcaatcca tcgaaatcga attgccaatg ggctatagcg aactcaagtt cacaagcctt
1500
tcgaaagacg gtatggcgaa catcgattac atcggctgga tgaacgatga tttgaaagtt
1560
ggcgaagttg aagtaccacg ctcatccatt gaagcaatac gcgccatccg caaagcccag
1620
caggacaacc gctactttgt ggactttggc ggcaacaata atagcgcagg ggcttacttt
1680
aagcgtggca tcaacacgtt ccgcgtgaat gggaagatga ggtaa
1725

<210> 118
<211> 574
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(24)

<221> DOMAIN
<222> (25)...(574)
<223> Catalytic domain

<400> 118
Met Lys Asn Phe Gly Phe Gly Asn Tyr Lys Phe Phe Val Ala Ala Met
 1   5   10   15
Ser Val Ala Ser Phe Ser Tyr Ala Ala Ser Tyr Thr Pro Pro Ser Thr
            20   25   30
Ala Val Ser Lys Ile Asn Ser Tyr Arg Gly Tyr Ser Glu Leu Thr Ser
        35   40   45
Ala Ala Ser Gly Met Asp Ile Asp Gln Tyr Thr Tyr Asn Met Thr Thr
    50   55   60
Trp Gln Ile Ala Asn Gly Gly Phe Tyr Lys Ala Met Ala Asp Lys Tyr

65 70 75 80
Lys Ser Ala Tyr Gly Gly Gly Gln Lys Ser Glu Trp Gln Ala Lys Gly
85 90 95
Gly Gly Asp Leu Gly Thr Ile Asp Asn Asn Ala Thr Ile Gln Glu Met
100 105 110
Arg Leu Leu Ala Val Arg Tyr Lys Glu Thr Thr Asn Asn Asn Tyr Lys
115 120 125
Ser Ala Phe Lys Thr Ser Phe Asn Lys Ala Val Asn Phe Leu Leu Thr
130 135 140
Met Gln Arg Ser Lys Gly Gly Leu Pro Gln Val Trp Pro Lys Arg Gly
145 150 155 160
Asn Tyr Ser Asp Gln Ile Thr Leu Asn Asp Asn Ala Met Ile Arg Ala
165 170 175
Met Val Thr Met Met Asp Ile Ala Asn Lys Thr Ser Pro Phe Asp Ser
180 185 190
Asp Ile Ile Asp Asp Ala Thr Arg Ser Lys Met Lys Ser Ala Leu Asp
195 200 205
Lys Ala Val Asp Tyr Leu Leu Lys Ala Gln Ile Val Asn Asp Gly Lys
210 215 220
Val Thr Val Trp Cys Ala Gln His Asp Thr Asn Ser Leu Ala Pro Val
225 230 235 240
Gly Ala Arg Ala Tyr Glu Leu Pro Ser Lys Ser Gly Asn Glu Ser Met
245 250 255
Gly Val Val Trp Phe Leu Met Asn Trp Pro Asp Gln Asn Glu Ala Ile
260 265 270
Gln Lys Ala Val Lys Gly Ala Ile Ala Trp Tyr Lys Lys Asn Lys Leu
275 280 285
Lys Asp Lys Ala Phe Ser Lys Thr Ala Gly Val Val Asp Lys Ala Gly
290 295 300
Ser Ser Leu Trp Phe Arg Phe Tyr Glu Val Asn Asn Asp Asn Tyr Phe
305 310 315 320
Phe Cys Asp Arg Asp Gly Ala Ser Thr Lys Thr Gln Asp Phe Met Lys
325 330 335
Ile Ser Glu Glu Arg Arg Lys Gly Tyr Gln Trp Ala Gly Asp Tyr Gly
340 345 350
Ser Ala Ile Leu Gly Thr Glu Asn Ala Tyr Leu Glu Ala Leu Ala Lys
355 360 365
Met Asp Asp Asn Tyr Val Pro Pro Pro Pro Ala Pro Ala Met Cys Gly
370 375 380
Asn Asp Thr Cys Lys Thr Tyr Ile Asp Gly Val Asp Phe Ile Asp Ile
385 390 395 400
Gln Gly Val Lys Glu Thr Thr Asn Thr Gly Phe Val Gly Glu Gly Tyr
405 410 415
Ala Asn Val Asp Asn Ser Thr Gly Ser Tyr Val Thr Tyr Gly Val Thr
420 425 430
Ala Phe Lys Glu Gly Lys Tyr Thr Leu Phe Ile Ser Phe Ala Asn Gly
435 440 445
Gly Gly Ser Ala Arg Gly Tyr Ser Val Ser Ala Gly Asp Lys Thr Leu
450 455 460
Leu Ala Asp Gly Ser Met Glu Ser Thr Ala Ala Trp Thr Thr Trp Lys
465 470 475 480
Met Gln Ser Ile Glu Ile Glu Leu Pro Met Gly Tyr Ser Glu Leu Lys
485 490 495
Phe Thr Ser Leu Ser Lys Asp Gly Met Ala Asn Ile Asp Tyr Ile Gly
500 505 510
Trp Met Asn Asp Asp Leu Lys Val Gly Glu Val Glu Val Pro Arg Ser
515 520 525
Ser Ile Glu Ala Ile Arg Ala Ile Arg Lys Ala Gln Gln Asp Asn Arg
530 535 540
Tyr Phe Val Asp Phe Gly Gly Asn Asn Asn Ser Ala Gly Ala Tyr Phe
545 550 555 560

Lys Arg Gly Ile Asn Thr Phe Arg Val Asn Gly Lys Met Arg
565 570

<210> 119
<211> 1848
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 119
gtgtcatggc aggaatccgg tgcggctatc accaacgcct ggaatgcaac gctcagtggc
60
tcaaaccctt acacagccgt atccgctggt tggaatggca cacttgcccc caatgcatcg
120
gccacttttg gtttccaggc aaacggttct gccggtgcac ctaaagtgaa tggcagcttg
180
tgcggcacca acacttcatc aacaccggca tccagcagtg ttgccagctc ggttaaatca
240
agcgcgcccg tatcgtccag cagcagatca tccagttcaa tcgctatcac tagcagctct
300
ttagcgagaa gttctattgc ctccagcagc tcactagtta gtagctccag agcgagcagt
360
agtgcgccaa gcgttttctc ttttacgatc caggaagagc aagcgggctt ctgtcgtgtt
420
gatggcattg cgacagaaag caccaacacc ggttttaccg gcaatggcta caccaatgcg
480
aacaacgcgc aaggcgcagc gattgaatgg gcagtcagcg cacctagcag tggccgttat
540
acagtagcct tccgcttcgc caatggcggc acagcagcgc gcaacggctc gttgttaatc
600
aatggcggta gcaatggtaa ttacactgtg gagttacccc tgaccggcgc atgggcaacc
660
tggcaaattg ccagcgtgga aattgattta gtgcaaggca ataatatttt aaaactctcg
720
gcgttaaccg ctgacggttt ggccaatatc gactcattaa aaatagacgg cgcgcaaacc
780
aaagcaggta cttgcagcac tacatcaagc agcagcgttg ccagcagctc gtcgtccgtt
840
aaatccagcg caagttcttc ttcgagttca tccaccgctg caaaaatact gacattagac
900
ggtaacccgg ccgccagctg gttcaacaaa tccaggacca agtggaatag cagccgcgcc
960
gatattgtgt tgtcttacca gcaatccaac ggcggttggc caaaaaacct ggattacaac
1020
tcagtgagcg caggcaatgg cgggagcgac agcggcacca tcgacaatgg tgcaaccatt
1080
accgaaatgg tttacctcgc tgaaatttat aaaaacggcg gcaacaccaa atatcgcgat
1140
gcagtgcgca gagcagcaaa ctttttagtg agctcgcaat acagcacagg cgccttgcca
1200
caattttatc cgttgaaagg cggctatgcg gatcatgcga cctttaacga taacggcatg
1260
gcgtacgcgt tgacggtatt ggatttcgca gtaaacaaac gcgcaccgtt tgataacgac
1320
attttctctg attctgatcg ggcgaaattc aaaaccgctg ttgccaaagg tgtggattac
1380
attttaaaag cgcagtggaa acaaaatgga aaactcactg catggtgtgc acaacacggt
1440
gctacggatt accaaccgaa aaaagcgcgc gcttatgaat tggaatcatt gagtggtagc

1500
gagtcggtcg gcattctcgc cttcttgatg acccaaccac aaaccgcgca aatcgaagcg
1560
gcggtcaagg cgggtgtcaa ctggttcgcc agtccaaata cttatttggc taactacact
1620
tacgattcat caaaagcgtc taccaacccg attgtgtata aatccggaag cagaatgtgg
1680
tatcgcttct atgacctgaa caccaaccgt ggtttcttta gtgatcgcga tggcagcaaa
1740
ttctatgata tcacccaaat gtcagaagag cgtcgcaccg gttatagctg gggtggctct
1800
tacggtgaat ctattatttc cttcgcgcaa aaagtgggtt atctgtaa
1848

<210> 120
<211> 615
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> BINDING
<222> (1)...(61)
<223> Carbohydrate binding module

<221> BINDING
<222> (134)...(257)
<223> Carbohydrate binding module

<221> DOMAIN
<222> (258)...(615)
<223> Catalytic domain

<400> 120
Met Ser Trp Gln Glu Ser Gly Ala Ala Ile Thr Asn Ala Trp Asn Ala
 1   5   10   15
Thr Leu Ser Gly Ser Asn Pro Tyr Thr Ala Val Ser Ala Gly Trp Asn
            20   25   30
Gly Thr Leu Ala Pro Asn Ala Ser Ala Thr Phe Gly Phe Gln Ala Asn
        35   40   45
Gly Ser Ala Gly Ala Pro Lys Val Asn Gly Ser Leu Cys Gly Thr Asn
    50   55   60
Thr Ser Ser Thr Pro Ala Ser Ser Ser Val Ala Ser Ser Val Lys Ser
65   70   75   80
Ser Ala Pro Val Ser Ser Ser Ser Arg Ser Ser Ser Ser Ile Ala Ile
                85   90   95
Thr Ser Ser Ser Leu Ala Arg Ser Ser Ile Ala Ser Ser Ser Ser Leu
            100   105   110
Val Ser Ser Ser Arg Ala Ser Ser Ser Ala Pro Ser Val Phe Ser Phe
        115   120   125
Thr Ile Gln Glu Glu Gln Ala Gly Phe Cys Arg Val Asp Gly Ile Ala
    130   135   140
Thr Glu Ser Thr Asn Thr Gly Phe Thr Gly Asn Gly Tyr Thr Asn Ala
145   150   155   160
Asn Asn Ala Gln Gly Ala Ala Ile Glu Trp Ala Val Ser Ala Pro Ser
                165   170   175
Ser Gly Arg Tyr Thr Val Ala Phe Arg Phe Ala Asn Gly Gly Thr Ala
            180   185   190
Ala Arg Asn Gly Ser Leu Leu Ile Asn Gly Gly Ser Asn Gly Asn Tyr
        195   200   205

Thr Val Glu Leu Pro Leu Thr Gly Ala Trp Ala Thr Trp Gln Ile Ala
210 215 220
Ser Val Glu Ile Asp Leu Val Gln Gly Asn Asn Ile Leu Lys Leu Ser
225 230 235 240
Ala Leu Thr Ala Asp Gly Leu Ala Asn Ile Asp Ser Leu Lys Ile Asp
245 250 255
Gly Ala Gln Thr Lys Ala Gly Thr Cys Ser Thr Thr Ser Ser Ser Ser
260 265 270
Val Ala Ser Ser Ser Ser Ser Val Lys Ser Ser Ala Ser Ser Ser Ser
275 280 285
Ser Ser Ser Thr Ala Ala Lys Ile Leu Thr Leu Asp Gly Asn Pro Ala
290 295 300
Ala Ser Trp Phe Asn Lys Ser Arg Thr Lys Trp Asn Ser Ser Arg Ala
305 310 315 320
Asp Ile Val Leu Ser Tyr Gln Gln Ser Asn Gly Gly Trp Pro Lys Asn
325 330 335
Leu Asp Tyr Asn Ser Val Ser Ala Gly Asn Gly Gly Ser Asp Ser Gly
340 345 350
Thr Ile Asp Asn Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala Glu
355 360 365
Ile Tyr Lys Asn Gly Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg Arg
370 375 380
Ala Ala Asn Phe Leu Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu Pro
385 390 395 400
Gln Phe Tyr Pro Leu Lys Gly Gly Tyr Ala Asp His Ala Thr Phe Asn
405 410 415
Asp Asn Gly Met Ala Tyr Ala Leu Thr Val Leu Asp Phe Ala Val Asn
420 425 430
Lys Arg Ala Pro Phe Asp Asn Asp Ile Phe Ser Asp Ser Asp Arg Ala
435 440 445
Lys Phe Lys Thr Ala Val Ala Lys Gly Val Asp Tyr Ile Leu Lys Ala
450 455 460
Gln Trp Lys Gln Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln His Gly
465 470 475 480
Ala Thr Asp Tyr Gln Pro Lys Lys Ala Arg Ala Tyr Glu Leu Glu Ser
485 490 495
Leu Ser Gly Ser Glu Ser Val Gly Ile Leu Ala Phe Leu Met Thr Gln
500 505 510
Pro Gln Thr Ala Gln Ile Glu Ala Ala Val Lys Ala Gly Val Asn Trp
515 520 525
Phe Ala Ser Pro Asn Thr Tyr Leu Ala Asn Tyr Thr Tyr Asp Ser Ser
530 535 540
Lys Ala Ser Thr Asn Pro Ile Val Tyr Lys Ser Gly Ser Arg Met Trp
545 550 555 560
Tyr Arg Phe Tyr Asp Leu Asn Thr Asn Arg Gly Phe Phe Ser Asp Arg
565 570 575
Asp Gly Ser Lys Phe Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg Arg
580 585 590
Thr Gly Tyr Ser Trp Gly Gly Ser Tyr Gly Glu Ser Ile Ile Ser Phe
595 600 605
Ala Gln Lys Val Gly Tyr Leu
610 615

<210> 121
<211> 1047
<212> DNA
<213> Bacteria

<400> 121
atgatgagat caagcatcgt caagctagtt gctttcagtg ttgtggttat gttatggctc
60

ggtgtatcct ttcaaacggc agaagcgaat acgccaaatt tcaacttaca aggctttgcc
120
acgttaaatg ggggaacaac tggtggtgca ggtggagatg tagtgacggt tcgtacaggg
180
aatgaattaa taaacgcttt gaagtccaaa aaccctaatc gtccgttaac aatttatgta
240
aacggtacga taacacctag taatacgtct gatagtaaga tcgatattaa ggatgtttcc
300
aatgtatcga ttttaggggt tggtacaaat ggacgattaa atgggatcgg tattaaagta
360
tggcgagcga ataatatcat cattcgcaac ttgacgatcc atgaagtcca tacaggtgat
420
aaagatgcga ttagcattga agggccctct cggaacattt ggattgacca taacgagctt
480
tatgccagct tgaacgttca taaagaccac tatgacggct tgtttgacgt aaagcgcgat
540
gcttacaata ttaccttctc ttggaattat gtccatgatg gctggaaagc gatgctcatg
600
gggaactctg atagtgataa ctacgaccga aacataacat tccaccataa ctacttcaaa
660
aacttaaact ctcgcgtacc tgcgtaccgt tttggaaagg cgcacttgtt tagcaattac
720
tttgagaaca ttttagaaac aggcattaat tcacggatgg gagcggaaat gctcgttgaa
780
cataacgttt ttgagaatgc caccaacccg ttaggattct ggcatagcag tcgaacaggt
840
tattggaatg ttgccaataa ccgctatatc aatagcacgg gtagcatgcc gaccacttcc
900
acgaccaatt atcgacctcc ttatccctat acggtcacac cagttggtga tgtgaaatcg
960
gttgtcacac gttatgcggg agttggtgtc atccagccgt atgcaagaaa gccatccgag
1020
cgattgctct ggtggctttt tgcataa
1047

<210> 122
<211> 348
<212> PRT
<213> Bacteria

<220>

<221> SIGNAL
<222> (1)...(29)

<221> DOMAIN
<222> (30)...(348)
<223> Catalytic domain

<400> 122
Met Met Arg Ser Ser Ile Val Lys Leu Val Ala Phe Ser Val Val Val
 1   5   10   15
Met Leu Trp Leu Gly Val Ser Phe Gln Thr Ala Glu Ala Asn Thr Pro
            20   25   30
Asn Phe Asn Leu Gln Gly Phe Ala Thr Leu Asn Gly Gly Thr Thr Gly
        35   40   45
Gly Ala Gly Gly Asp Val Val Thr Val Arg Thr Gly Asn Glu Leu Ile
    50   55   60
Asn Ala Leu Lys Ser Lys Asn Pro Asn Arg Pro Leu Thr Ile Tyr Val
65   70   75   80
Asn Gly Thr Ile Thr Pro Ser Asn Thr Ser Asp Ser Lys Ile Asp Ile

```
                85                  90                  95
Lys Asp Val Ser Asn Val Ser Ile Leu Gly Val Gly Thr Asn Gly Arg
            100                 105                 110
Leu Asn Gly Ile Gly Ile Lys Val Trp Arg Ala Asn Asn Ile Ile Ile
        115                 120                 125
Arg Asn Leu Thr Ile His Glu Val His Thr Gly Asp Lys Asp Ala Ile
    130                 135                 140
Ser Ile Glu Gly Pro Ser Arg Asn Ile Trp Ile Asp His Asn Glu Leu
145                 150                 155                 160
Tyr Ala Ser Leu Asn Val His Lys Asp His Tyr Asp Gly Leu Phe Asp
                165                 170                 175
Val Lys Arg Asp Ala Tyr Asn Ile Thr Phe Ser Trp Asn Tyr Val His
            180                 185                 190
Asp Gly Trp Lys Ala Met Leu Met Gly Asn Ser Asp Ser Asp Asn Tyr
        195                 200                 205
Asp Arg Asn Ile Thr Phe His His Asn Tyr Phe Lys Asn Leu Asn Ser
    210                 215                 220
Arg Val Pro Ala Tyr Arg Phe Gly Lys Ala His Leu Phe Ser Asn Tyr
225                 230                 235                 240
Phe Glu Asn Ile Leu Glu Thr Gly Ile Asn Ser Arg Met Gly Ala Glu
                245                 250                 255
Met Leu Val Glu His Asn Val Phe Glu Asn Ala Thr Asn Pro Leu Gly
            260                 265                 270
Phe Trp His Ser Ser Arg Thr Gly Tyr Trp Asn Val Ala Asn Asn Arg
        275                 280                 285
Tyr Ile Asn Ser Thr Gly Ser Met Pro Thr Thr Ser Thr Thr Asn Tyr
    290                 295                 300
Arg Pro Pro Tyr Pro Tyr Thr Val Thr Pro Val Gly Asp Val Lys Ser
305                 310                 315                 320
Val Val Thr Arg Tyr Ala Gly Val Gly Val Ile Gln Pro Tyr Ala Arg
                325                 330                 335
Lys Pro Ser Glu Arg Leu Leu Trp Trp Leu Phe Ala
            340                 345
```

<210> 123
<211> 1830
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 123
ttgagtctac ttagtgtaat gacccttttg cctgtaatgg caagtaacaa cgtagctccc
60
tggggctggg ccacctgctc cgatgagtca gcgacagctt atactctgaa cggaggttgc
120
ttttctgatg catcttccgt tactctgaaa gctcttggca atgaacaaac agatgacaaa
180
caaatcaaac aggctatcgc tcagaaagac atcattatct tagatggttc caatggcgat
240
ttcatcctta atgaatacat caagatttcg accaaaaaca aaaccatcat tggtatcaac
300
aacgcccgcc tgtgtacaaa gttctaccta accgctgatg atattacgta ccttaaagca
360
caaggactgg agggactgag tagtacaaat caacatacag gaactctgcc tgatggcaca
420
acagtgacct gtgacgagcg tgccttttc accaagaaag ccatcatgga actccaatat
480
cagaaaacag gatcctatac cctacccaat aaatcaggta tcttttattt agatgccgct
540

tctgagaata tcatcatccg aaatatttcg ctgatagggc caggagccgt agatatagac
600
ggagctgacc tgattaccaa tcagggtaag cacgtctgga ttgaccattg cacgtttgtg
660
gactctcaag atggtgccct ggacagcaag gtatgcgact gggccaccta tacctataac
720
cacttctact atacagaccg cagttactca catgcctaca cttgcggttg cggatgggtc
780
agcaatcatg aaatggtgat tcacatgacc tttgcatgta atatctgggg agcaaaatgt
840
atgcgtcgtc tgccgcaagc agatgactgt ttcatacacc ttgtgaacaa ctatcacaac
900
tgtcctggca atagtgtcgg tatgaccatt aacagttaca gcaaagcatt ggttgagggt
960
aactatgctg ctgcaggtgt caacaagcca ttagatggca gtggggccaa ccgtaatgta
1020
acagctaagg ataatagttt tgcaaactca caagccggtt ctgttgtgtc tgtgccatac
1080
gactatacca agattgcagc cgccgacgtt ccagctacgc tgactggaac agagggtgca
1140
ggcgccacat taggcaacga tgcaacatac attctgtcta ctattccaac tgtcgaccga
1200
caagaaggcg aatcttcact ctactatttc attgatggcc tggtgggaac taatagtgaa
1260
ggctattcca ttatagagtt taatgatggc gcaacattgc tgctgaacaa taaagagaaa
1320
gcatggtcta atggtagtgc aattcaactt ggtgacgata attatacgag tattaaactt
1380
tctaatggag cagaaaacat cttcacagca cctactggca aaaaagtaag tggtattacc
1440
ttctattctt atatcaatat aaaagaagaa aaactcgact tcaccaaata tccagaatat
1500
ggtttccgca cctgtttctg gcagaaagtt gccaacctca cttattctgc gacttctgat
1560
gacgtacaaa tcttgaaatc tcgtgatcca cagaatactg acgtggcatc attccatttc
1620
actccaacaa atgttgtaag tttcaaaaat tcaggtgaac agctttgttt cttaatgaaa
1680
gtcacctata gtgatgaaag cacaggtatc tctgctatcc agaaaaaaat gcctatcgat
1740
ggcgttacct ataaccttca aggtatccgt atagataatc ccaccaaggg aatctatatt
1800
cagaacggaa agaaaatcat tatcaaataa
1830

<210> 124
<211> 609
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(21)

<221> DOMAIN
<222> (22)...(390)
<223> Catalytic domain

<400> 124

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Leu Ser Leu Leu Ser Val Met Thr Leu Leu Pro Val Met Ala Ser Asn
 1               5                  10                  15
Asn Val Ala Pro Trp Gly Trp Ala Thr Cys Ser Asp Glu Ser Ala Thr
            20                  25                  30
Ala Tyr Thr Leu Asn Gly Gly Cys Phe Ser Asp Ala Ser Ser Val Thr
        35                  40                  45
Leu Lys Ala Leu Gly Asn Glu Gln Thr Asp Asp Lys Gln Ile Lys Gln
    50                  55                  60
Ala Ile Ala Gln Lys Asp Ile Ile Ile Leu Asp Gly Ser Asn Gly Asp
65                  70                  75                  80
Phe Ile Leu Asn Glu Tyr Ile Lys Ile Ser Thr Lys Asn Lys Thr Ile
                85                  90                  95
Ile Gly Ile Asn Asn Ala Arg Leu Cys Thr Lys Phe Tyr Leu Thr Ala
            100                 105                 110
Asp Asp Ile Thr Tyr Leu Lys Ala Gln Gly Leu Glu Gly Leu Ser Ser
        115                 120                 125
Thr Asn Gln His Thr Gly Thr Leu Pro Asp Gly Thr Thr Val Thr Cys
    130                 135                 140
Asp Glu Arg Ala Phe Phe Thr Lys Lys Ala Ile Met Glu Leu Gln Tyr
145                 150                 155                 160
Gln Lys Thr Gly Ser Tyr Thr Leu Pro Asn Lys Ser Gly Ile Phe Tyr
                165                 170                 175
Leu Asp Ala Ala Ser Glu Asn Ile Ile Ile Arg Asn Ile Ser Leu Ile
            180                 185                 190
Gly Pro Gly Ala Val Asp Ile Asp Gly Ala Asp Leu Ile Thr Asn Gln
        195                 200                 205
Gly Lys His Val Trp Ile Asp His Cys Thr Phe Val Asp Ser Gln Asp
    210                 215                 220
Gly Ala Leu Asp Ser Lys Val Cys Asp Trp Ala Thr Tyr Thr Tyr Asn
225                 230                 235                 240
His Phe Tyr Tyr Thr Asp Arg Ser Tyr Ser His Ala Tyr Thr Cys Gly
                245                 250                 255
Cys Gly Trp Val Ser Asn His Glu Met Val Ile His Met Thr Phe Ala
            260                 265                 270
Cys Asn Ile Trp Gly Ala Lys Cys Met Arg Arg Leu Pro Gln Ala Asp
        275                 280                 285
Asp Cys Phe Ile His Leu Val Asn Asn Tyr His Asn Cys Pro Gly Asn
    290                 295                 300
Ser Val Gly Met Thr Ile Asn Ser Tyr Ser Lys Ala Leu Val Glu Gly
305                 310                 315                 320
Asn Tyr Ala Ala Ala Gly Val Asn Lys Pro Leu Asp Gly Ser Gly Ala
                325                 330                 335
Asn Arg Asn Val Thr Ala Lys Asp Asn Ser Phe Ala Asn Ser Gln Ala
            340                 345                 350
Gly Ser Val Val Ser Val Pro Tyr Asp Tyr Thr Lys Ile Ala Ala Ala
        355                 360                 365
Asp Val Pro Ala Thr Leu Thr Gly Thr Glu Gly Ala Gly Ala Thr Leu
    370                 375                 380
Gly Asn Asp Ala Thr Tyr Ile Leu Ser Thr Ile Pro Thr Val Asp Arg
385                 390                 395                 400
Gln Glu Gly Glu Ser Ser Leu Tyr Tyr Phe Ile Asp Gly Leu Val Gly
                405                 410                 415
Thr Asn Ser Glu Gly Tyr Ser Ile Ile Glu Phe Asn Asp Gly Ala Thr
            420                 425                 430
Leu Leu Leu Asn Asn Lys Glu Lys Ala Trp Ser Asn Gly Ser Ala Ile
        435                 440                 445
Gln Leu Gly Asp Asp Asn Tyr Thr Ser Ile Lys Leu Ser Asn Gly Ala
    450                 455                 460
Glu Asn Ile Phe Thr Ala Pro Thr Gly Lys Lys Val Ser Gly Ile Thr
465                 470                 475                 480
Phe Tyr Ser Tyr Ile Asn Ile Lys Glu Glu Lys Leu Asp Phe Thr Lys
```

485 490 495
Tyr Pro Glu Tyr Gly Phe Arg Thr Cys Phe Trp Gln Lys Val Ala Asn
500 505 510
Leu Thr Tyr Ser Ala Thr Ser Asp Asp Val Gln Ile Leu Lys Ser Arg
515 520 525
Asp Pro Gln Asn Thr Asp Val Ala Ser Phe His Phe Thr Pro Thr Asn
530 535 540
Val Val Ser Phe Lys Asn Ser Gly Glu Gln Leu Cys Phe Leu Met Lys
545 550 555 560
Val Thr Tyr Ser Asp Glu Ser Thr Gly Ile Ser Ala Ile Gln Lys Lys
565 570 575
Met Pro Ile Asp Gly Val Thr Tyr Asn Leu Gln Gly Ile Arg Ile Asp
580 585 590
Asn Pro Thr Lys Gly Ile Tyr Ile Gln Asn Gly Lys Lys Ile Ile Ile
595 600 605
Lys

<210> 125
<211> 1170
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 125
atgaggtcta aaatcatcag cgccataaat aattatagtg ttattattct cgatggctcg
60
aatggcgatt tcactattag tgctacaatg agtttcagta gcaaatcaaa caaaaccata
120
gttggtgtaa ataatgctcg cctatgcacc aagttctatc taaccgatga aataaagact
180
gcgctcgatg ctgctaatgt aaaatcagca agttcaacca gtggaggtgg tacactctca
240
aatgggaaat cagtgtcaga acaacgtgaa taccttactc gtcaaacaat tatcgatcta
300
actggcgatg cttcggaatc gtgtcagaaa gcgggcatct ttagcttcag tagttgtacc
360
aatatcatca tgcgaaacct cgttttggtt ggccctggcc catgcgatgt aggtggcaac
420
gatttgcttt cgctcactgg ttctaagcat ttttgggtcg atcactgtga gttaaccgat
480
ggtatagatg gcaatttcga tattaccaag agtagcgatt tcaatactgt tacttggtgt
540
atattcaatt ataccgatcg tgcatacgac cacatgaact ccaatcttat tggtagctcc
600
gatagcgaag atgctgccta tttgaacact actatggcat gcaatatttg gggctacaag
660
tgcaatcagc gaatgccaat ggctcgtgct ggtaatattc accttgtgaa caacttttac
720
gattgcgctg gcaatagtgt ggctgttaac cctcgtaaaa attctgagtt cttagtcgag
780
aactgctact ttgccacggg tgtgaagcca ttctcgcaga gtggtgcgtt gggatacaac
840
tttattgatt gctatacaga agattcatac acttttcagc agagtggtac agtgtctgtg
900
ccatacgttt actctaagtt tgatgtgcaa ttagtacccg agcaactcaa taaatatgct
960
ggcgcaacgc ttacttctcc gcttgtcata ggtcgggaag agggtgttgt tactcctatt
1020

agtgctgtct ctgttgatag cgatgttgtg ttggtcgaat actattcgct gactggtaat
1080
cgtgttaaca cgctcaatag aggcatcaat atcgttagaa ctatttacgc caacggcaaa
1140
gtaaccacac aaaaggtttt ggtgaaatag
1170

<210> 126
<211> 389
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> DOMAIN
<222> (24)...(325)
<223> Catalytic domain

<400> 126
Met Arg Ser Lys Ile Ile Ser Ala Ile Asn Asn Tyr Ser Val Ile Ile
 1   5   10   15
Leu Asp Gly Ser Asn Gly Asp Phe Thr Ile Ser Ala Thr Met Ser Phe
            20   25   30
Ser Ser Lys Ser Asn Lys Thr Ile Val Gly Val Asn Asn Ala Arg Leu
        35   40   45
Cys Thr Lys Phe Tyr Leu Thr Asp Glu Ile Lys Thr Ala Leu Asp Ala
    50   55   60
Ala Asn Val Lys Ser Ala Ser Ser Thr Ser Gly Gly Gly Thr Leu Ser
65   70   75   80
Asn Gly Lys Ser Val Ser Glu Gln Arg Glu Tyr Leu Thr Arg Gln Thr
                85   90   95
Ile Ile Asp Leu Thr Gly Asp Ala Ser Glu Ser Cys Gln Lys Ala Gly
            100   105   110
Ile Phe Ser Phe Ser Ser Cys Thr Asn Ile Ile Met Arg Asn Leu Val
        115   120   125
Leu Val Gly Pro Gly Pro Cys Asp Val Gly Gly Asn Asp Leu Leu Ser
    130   135   140
Leu Thr Gly Ser Lys His Phe Trp Val Asp His Cys Glu Leu Thr Asp
145   150   155   160
Gly Ile Asp Gly Asn Phe Asp Ile Thr Lys Ser Ser Asp Phe Asn Thr
                165   170   175
Val Thr Trp Cys Ile Phe Asn Tyr Thr Asp Arg Ala Tyr Asp His Met
            180   185   190
Asn Ser Asn Leu Ile Gly Ser Ser Asp Ser Glu Asp Ala Ala Tyr Leu
        195   200   205
Asn Thr Thr Met Ala Cys Asn Ile Trp Gly Tyr Lys Cys Asn Gln Arg
    210   215   220
Met Pro Met Ala Arg Ala Gly Asn Ile His Leu Val Asn Asn Phe Tyr
225   230   235   240
Asp Cys Ala Gly Asn Ser Val Ala Val Asn Pro Arg Lys Asn Ser Glu
                245   250   255
Phe Leu Val Glu Asn Cys Tyr Phe Ala Thr Gly Val Lys Pro Phe Ser
            260   265   270
Gln Ser Gly Ala Leu Gly Tyr Asn Phe Ile Asp Cys Tyr Thr Glu Asp
        275   280   285
Ser Tyr Thr Phe Gln Gln Ser Gly Thr Val Ser Val Pro Tyr Val Tyr
    290   295   300
Ser Lys Phe Asp Val Gln Leu Val Pro Glu Gln Leu Asn Lys Tyr Ala
305   310   315   320
Gly Ala Thr Leu Thr Ser Pro Leu Val Ile Gly Arg Glu Glu Gly Val

325 330 335
Val Thr Pro Ile Ser Ala Val Ser Val Asp Ser Asp Val Val Leu Val
340 345 350
Glu Tyr Tyr Ser Leu Thr Gly Asn Arg Val Asn Thr Leu Asn Arg Gly
355 360 365
Ile Asn Ile Val Arg Thr Ile Tyr Ala Asn Gly Lys Val Thr Thr Gln
370 375 380
Lys Val Leu Val Lys
385

<210> 127
<211> 1449
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<400> 127
atgcaatatg gcaaattagt acgcttgtcg gcactgacaa cagcgctggc attcagcgcc
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ctggcacagg caaataacct ggcaattaca ggccccggag ccggggctga tggttccagc
120
aaagccagtg gcagtagcta cggcgatgta aaagacgccg atctgcaaag ctactggcaa
180
ccgcctgcta ataacggcca aagagtgtcg gttaagtgga gcagcgctat cagcgttaat
240
caggtaatac tgcgtgaaca gggcagtaat gtaaccagct ggcggctggt aaataatgac
300
aacggcgcag tattggcaac cggcaccagc attggcagca acagaacggt taacttcagc
360
actgtaagca cgaaaaaact caatctggaa atactaactg ccagcggtgc cccgcgcatt
420
gctgagtttg aagtttattt aaataccaat ggcggcaacc cgccaaatcc tactgacccg
480
gaaccaggcc cggtaacttc ttgcgcagcg tctccacagg gctatgcctc gcttaacggt
540
ggcactaccg gcggcagtgg cagcaacgcg gtcacggtaa cggtaagcac cggcgctcaa
600
atggtatcgg cgctacaaaa ccgcgatcta aaccggccgc tcactatccg ggttaatggc
660
actatcacac cgggtaattc tggcggtgtc agtaagtttg acattaaaga tatggataat
720
gtcagcatta ttggtgtagg caacaatgcg ttgtttgacg gtatcggtat taaaatctgg
780
cgggccaata acgttattat ccgcaacctt acaatgcgtt atgttaacac cggcgataaa
840
gacgctatta ccattgaagg cccggcgcgt aatatctgga ttgaccacaa cgaaatctat
900
aacagcctga atgtgggtaa agatttttac gacgagctta taagcggtaa aaaagacgta
960
gataacgtaa ctatctctta caactacctg cacgacagct ggaaaacctc gctgtggggc
1020
agcagtgatt ccgacaacta caaccgccgt attacctttc accataacca ctggcataag
1080
gtaaattcac gcctgccact gttccgtttt ggccagggcc atatttacaa taactattac
1140
aacgacattc aggacaccgg tattaacagc cggatgggtg cggtaattcg tattgaaaac
1200
aatgtgtttg aaaacgcgaa aaacccgata gtgtcgtttt attccagcgg ctacggttac
1260

tgggacaccc gcggtaatag ctttagcaat attacctggc aggaataccc cagcgacggc
1320
attatcgccg ggccaaatgt acaacccaca gcggtgctaa acctgcccta cagctttaac
1380
ctgttaccca ccaaccaggt aaaagcccac gtactggcca acgccggcgt gaataaatgt
1440
agtttctaa
1449

<210> 128
<211> 482
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample.

<221> SIGNAL
<222> (1)...(24)

<221> DOMAIN
<222> (5)...(482)
<223> Catalytic domain

<400> 128
Met Gln Tyr Gly Lys Leu Val Arg Leu Ser Ala Leu Thr Thr Ala Leu
 1   5   10   15
Ala Phe Ser Ala Leu Ala Gln Ala Asn Asn Leu Ala Ile Thr Gly Pro
            20   25   30
Gly Ala Gly Ala Asp Gly Ser Ser Lys Ala Ser Gly Ser Ser Tyr Gly
        35   40   45
Asp Val Lys Asp Ala Asp Leu Gln Ser Tyr Trp Gln Pro Pro Ala Asn
    50   55   60
Asn Gly Gln Arg Val Ser Val Lys Trp Ser Ser Ala Ile Ser Val Asn
65   70   75   80
Gln Val Ile Leu Arg Glu Gln Gly Ser Asn Val Thr Ser Trp Arg Leu
                85   90   95
Val Asn Asn Asp Asn Gly Ala Val Leu Ala Thr Gly Thr Ser Ile Gly
            100   105   110
Ser Asn Arg Thr Val Asn Phe Ser Thr Val Ser Thr Lys Lys Leu Asn
        115   120   125
Leu Glu Ile Leu Thr Ala Ser Gly Ala Pro Arg Ile Ala Glu Phe Glu
    130   135   140
Val Tyr Leu Asn Thr Asn Gly Gly Asn Pro Pro Asn Pro Thr Asp Pro
145   150   155   160
Glu Pro Gly Pro Val Thr Ser Cys Ala Ala Ser Pro Gln Gly Tyr Ala
                165   170   175
Ser Leu Asn Gly Gly Thr Thr Gly Gly Ser Gly Ser Asn Ala Val Thr
            180   185   190
Val Thr Val Ser Thr Gly Ala Gln Met Val Ser Ala Leu Gln Asn Arg
        195   200   205
Asp Leu Asn Arg Pro Leu Thr Ile Arg Val Asn Gly Thr Ile Thr Pro
    210   215   220
Gly Asn Ser Gly Gly Val Ser Lys Phe Asp Ile Lys Asp Met Asp Asn
225   230   235   240
Val Ser Ile Ile Gly Val Gly Asn Asn Ala Leu Phe Asp Gly Ile Gly
                245   250   255
Ile Lys Ile Trp Arg Ala Asn Asn Val Ile Ile Arg Asn Leu Thr Met
            260   265   270
Arg Tyr Val Asn Thr Gly Asp Lys Asp Ala Ile Thr Ile Glu Gly Pro
        275   280   285

Ala Arg Asn Ile Trp Ile Asp His Asn Glu Ile Tyr Asn Ser Leu Asn
290 295 300
Val Gly Lys Asp Phe Tyr Asp Glu Leu Ile Ser Gly Lys Lys Asp Val
305 310 315 320
Asp Asn Val Thr Ile Ser Tyr Asn Tyr Leu His Asp Ser Trp Lys Thr
325 330 335
Ser Leu Trp Gly Ser Ser Asp Ser Asp Asn Tyr Asn Arg Arg Ile Thr
340 345 350
Phe His His Asn His Trp His Lys Val Asn Ser Arg Leu Pro Leu Phe
355 360 365
Arg Phe Gly Gln Gly His Ile Tyr Asn Asn Tyr Tyr Asn Asp Ile Gln
370 375 380
Asp Thr Gly Ile Asn Ser Arg Met Gly Ala Val Ile Arg Ile Glu Asn
385 390 395 400
Asn Val Phe Glu Asn Ala Lys Asn Pro Ile Val Ser Phe Tyr Ser Ser
405 410 415
Gly Tyr Gly Tyr Trp Asp Thr Arg Gly Asn Ser Phe Ser Asn Ile Thr
420 425 430
Trp Gln Glu Tyr Pro Ser Asp Gly Ile Ile Ala Gly Pro Asn Val Gln
435 440 445
Pro Thr Ala Val Leu Asn Leu Pro Tyr Ser Phe Asn Leu Leu Pro Thr
450 455 460
Asn Gln Val Lys Ala His Val Leu Ala Asn Ala Gly Val Asn Lys Cys
465 470 475 480
Ser Phe

<210> 129
<211> 1173
<212> DNA
<213> Bacillus halodurans ATCC 27557

<220>

<400> 129
atgagttcga aaatcaaaaa tgctatcaat aactatagtg ttattattct cgatggctcg
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aatggcgatt ttacagtcaa tgctacaatg agtttcagtg gcaagtccaa taaaactatt
120
gtgggtgtga acaatgctcg cctatgcacc aaattctaca ttacgcccga gataaaagaa
180
gccctcgatg ctgccgatgt gaaatctaag agctcaagta gtggcactgg tggaactctt
240
tctaatggta cgtcggtcag tgaggctcgc gaattggcta ctcgtcaaac gttgattgat
300
tatctcggcg atagctcaga atcgtatcag aaagctggta tctttggctt tagcaactgc
360
actaatatta ttatgcgcaa cattgttttc gttggccctg gtccatgcga tgtaggtggc
420
aacgacttgc tttcgctcgt tggttcgaag catttctggg tcgaccactg cgagtttacc
480
gatggcatcg atggcaactt cgacatcacc aagagtagcg acttcaacac cgtttcgtgg
540
tgcactttca gctataccga ccgcgcatac gaccacatga attccaacct tattggtagc
600
tccgattcag agaatgcggc ttaccttaat actactatgg cttccaacgt ctggggcaat
660
aagtgcaatc agcgtatgcc tatggctcgt gccggtaata ttcacctcgt aaataattat
720
tacaactgcc ctggcaatag cgtggctgtg aatcctcgca aaaactcaga atttttggtg
780

gagaattgct atttcgcaag tggcgttaag cctttctcgc agagcggcgc tcttagctat
840
ctatttatcg attgctacac cgaagatact tacaccttcc agaaatctgg ctctactacg
900
gtgccataca catatagcaa attcgatgct cagcttgttc ccgagcaact cacccaattc
960
gctggcgcaa cattgacttc gccgcttgtt attggtaggg aatctgagaa tgttacacca
1020
gtctcagtca ttgctgcaaa tagcgatgtc atatctgtag aatactattc gctcactggc
1080
aagcgcatca gcgaaccaac taaaggcatc aatatcgtta gaactattta tactaacggc
1140
aacgtgacca cacaaaaggt cttggtgaaa taa
1173

<210> 130
<211> 390
<212> PRT
<213> Bacillus halodurans ATCC 27557

<220>

<221> DOMAIN
<222> (38)...(326)
<223> Catalytic domain

<400> 130
Met Ser Ser Lys Ile Lys Asn Ala Ile Asn Asn Tyr Ser Val Ile Ile
 1   5   10   15
Leu Asp Gly Ser Asn Gly Asp Phe Thr Val Asn Ala Thr Met Ser Phe
            20   25   30
Ser Gly Lys Ser Asn Lys Thr Ile Val Gly Val Asn Asn Ala Arg Leu
        35   40   45
Cys Thr Lys Phe Tyr Ile Thr Pro Glu Ile Lys Glu Ala Leu Asp Ala
    50   55   60
Ala Asp Val Lys Ser Lys Ser Ser Ser Ser Gly Thr Gly Gly Thr Leu
65   70   75   80
Ser Asn Gly Thr Ser Val Ser Glu Ala Arg Glu Leu Ala Thr Arg Gln
                85   90   95
Thr Leu Ile Asp Tyr Leu Gly Asp Ser Ser Glu Ser Tyr Gln Lys Ala
            100   105   110
Gly Ile Phe Gly Phe Ser Asn Cys Thr Asn Ile Ile Met Arg Asn Ile
        115   120   125
Val Phe Val Gly Pro Gly Pro Cys Asp Val Gly Gly Asn Asp Leu Leu
    130   135   140
Ser Leu Val Gly Ser Lys His Phe Trp Val Asp His Cys Glu Phe Thr
145   150   155   160
Asp Gly Ile Asp Gly Asn Phe Asp Ile Thr Lys Ser Ser Asp Phe Asn
                165   170   175
Thr Val Ser Trp Cys Thr Phe Ser Tyr Thr Asp Arg Ala Tyr Asp His
            180   185   190
Met Asn Ser Asn Leu Ile Gly Ser Ser Asp Ser Glu Asn Ala Ala Tyr
        195   200   205
Leu Asn Thr Thr Met Ala Ser Asn Val Trp Gly Asn Lys Cys Asn Gln
    210   215   220
Arg Met Pro Met Ala Arg Ala Gly Asn Ile His Leu Val Asn Asn Tyr
225   230   235   240
Tyr Asn Cys Pro Gly Asn Ser Val Ala Val Asn Pro Arg Lys Asn Ser
                245   250   255
Glu Phe Leu Val Glu Asn Cys Tyr Phe Ala Ser Gly Val Lys Pro Phe
            260   265   270

Ser Gln Ser Gly Ala Leu Ser Tyr Leu Phe Ile Asp Cys Tyr Thr Glu
275 280 285
Asp Thr Tyr Thr Phe Gln Lys Ser Gly Ser Thr Thr Val Pro Tyr Thr
290 295 300
Tyr Ser Lys Phe Asp Ala Gln Leu Val Pro Glu Gln Leu Thr Gln Phe
305 310 315 320
Ala Gly Ala Thr Leu Thr Ser Pro Leu Val Ile Gly Arg Glu Ser Glu
325 330 335
Asn Val Thr Pro Val Ser Val Ile Ala Ala Asn Ser Asp Val Ile Ser
340 345 350
Val Glu Tyr Tyr Ser Leu Thr Gly Lys Arg Ile Ser Glu Pro Thr Lys
355 360 365
Gly Ile Asn Ile Val Arg Thr Ile Tyr Thr Asn Gly Asn Val Thr Thr
370 375 380
Gln Lys Val Leu Val Lys
385 390

<210> 131
<211> 972
<212> DNA
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 131
atggcaaaaa tactgacatt agacggtaac ccggccgcca gctggttcaa caaatccagg
60
accaagtgga atagcagccg cgccgatatt gtgttgtctt accagcaatc caacggcggt
120
tggccaaaaa acctggatta caactcagtg agcgcaggca atggcgggag cgacagcggc
180
accatcgaca atggtgcaac cattaccgaa atggtttacc tcgctgaaat ttataaaaac
240
ggcggcaaca ccaaatatcg cgatgcagtg cgcagagcag caaacttttt agtgagctcg
300
caatacagca caggcgcctt gccacaattt tatccgttga aaggcggcta tgcggatcat
360
gcgaccttta acgataacgg catggcgtac gcgttgacgg tattggattt cgcagtaaac
420
aaacgcgcac cgtttgataa cgacattttc tctgattctg atcgggcgaa attcaaaacc
480
gctgttgcca aaggtgtgga ttacatttta aaagcgcagt ggaaacaaaa tggaaaactc
540
actgcatggt gtgcacaaca cggtgctacg gattaccaac cgaaaaaagc gcgcgcttat
600
gaattggaat cattgagtgg tagcgagtcg gtcggcattc tcgccttctt gatgacccaa
660
ccacaaaccg cgcaaatcga agcggcggtc aaggcgggtg tcaactggtt cgccagtcca
720
aatacttatt tggctaacta cacttacgat tcatcaaaag cgtctaccaa cccgattgtg
780
tataaatccg gaagcagaat gtggtatcgc ttctatgacc tgaacaccaa ccgtggtttc
840
tttagtgatc gcgatggcag caaattctat gatatcaccc aaatgtcaga agagcgtcgc
900
accggttata gctggggtgg ctcttacggt gaatctatta tttccttcgc gcaaaaagtg
960
ggttatctgt ag
972

<210> 132
<211> 323
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample

<400> 132
Met Ala Lys Ile Leu Thr Leu Asp Gly Asn Pro Ala Ala Ser Trp Phe
1 5 10 15
Asn Lys Ser Arg Thr Lys Trp Asn Ser Ser Arg Ala Asp Ile Val Leu
20 25 30
Ser Tyr Gln Gln Ser Asn Gly Gly Trp Pro Lys Asn Leu Asp Tyr Asn
35 40 45
Ser Val Ser Ala Gly Asn Gly Gly Ser Asp Ser Gly Thr Ile Asp Asn
50 55 60
Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala Glu Ile Tyr Lys Asn
65 70 75 80
Gly Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg Arg Ala Ala Asn Phe
85 90 95
Leu Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu Pro Gln Phe Tyr Pro
100 105 110
Leu Lys Gly Gly Tyr Ala Asp His Ala Thr Phe Asn Asp Asn Gly Met
115 120 125
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Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln His Gly Ala Thr Asp Tyr
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Gln Pro Lys Lys Ala Arg Ala Tyr Glu Leu Glu Ser Leu Ser Gly Ser
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Glu Ser Val Gly Ile Leu Ala Phe Leu Met Thr Gln Pro Gln Thr Ala
210 215 220
Gln Ile Glu Ala Ala Val Lys Ala Gly Val Asn Trp Phe Ala Ser Pro
225 230 235 240
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260 265 270
Asp Leu Asn Thr Asn Arg Gly Phe Phe Ser Asp Arg Asp Gly Ser Lys
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Ser Val Ser Ala Gly Asn Gly Gly Ser Asp Ser Gly Thr Ile Asp Asn
    50   55   60
Gly Ala Thr Ile Thr Glu Met Val Tyr Leu Ala Glu Ile Tyr Lys Asn
65   70   75   80
Gly Gly Asn Thr Lys Tyr Arg Asp Ala Val Arg Arg Ala Ala Asn Phe
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Leu Val Ser Ser Gln Tyr Ser Thr Gly Ala Leu Pro Gln Phe Tyr Pro
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Asn Gly Lys Leu Thr Ala Trp Cys Ala Gln His Gly Ala Leu Asp Tyr
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Gln Pro Lys Lys Gly Arg Ala Tyr Glu Leu Glu Ser Leu Ser Gly Lys
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Glu Ser Val Gly Ile Leu Ala Phe Leu Met Thr Gln Pro Gln Thr Ala
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Gln Ile Glu Ala Ala Val Lys Ala Gly Val Asn Trp Phe Ala Ser Pro
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Asn Thr Tyr Leu Ala Asn Tyr Thr Tyr Asp Ser Ser Lys Ala Ser Thr
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Phe Tyr Asp Ile Thr Gln Met Ser Glu Glu Arg Arg Thr Gly Tyr Ser
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Gly Tyr Leu
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